

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 11:34:39 / Search time 28 Seconds
(without alignments)
497.153 Million cell updates/sec

Title: US-10-004-176-6

Sequence: 1 VASGIGPEVPPDRDFEPL.....QPSTRCVYVRSALQLGNK 329

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1709	99.8	333	1 US-08-442-063A-27	Sequence 27, App1
2	1709	99.8	359	1 US-08-303-238-4	Sequence 4, App1
3	1709	99.8	359	3 US-08-458-834-4	Sequence 4, App1
4	1704	99.5	342	1 US-08-372-919-2	Sequence 2, App1
5	1704	99.5	342	1 US-08-619-916-2	Sequence 2, App1
6	1704	99.5	342	5 PCT-US95-08542-2	Sequence 2, App1
7	1653	96.5	353	6 5340934-4	Patent No. 5340934
8	1567	91.5	307	1 US-08-442-063A-48	Sequence 48, App1
9	1433	83.7	282	1 US-08-442-063A-45	Sequence 45, App1
10	1186	69.2	236	1 US-08-442-063A-42	Sequence 42, App1
11	966	56.4	358	3 US-08-303-238-3	Sequence 3, App1
12	966	56.4	358	3 US-08-458-834-3	Sequence 3, App1
13	966	56.3	368	6 5340934-2	Patent No. 5340934
14	948	55.3	188	1 US-08-442-063A-39	Sequence 39, App1
15	925.5	54.0	373	4 US-09-724-864-43	Sequence 43, App1
16	714	41.7	141	1 US-08-442-063A-36	Sequence 36, App1
17	488	28.5	96	1 US-08-442-063A-33	Sequence 33, App1
18	341	19.9	649	3 US-09-188-930-303	Sequence 305, App
19	341	19.9	649	4 US-09-312-283C-305	Sequence 305, App
20	326.5	19.1	376	3 US-08-303-238-1	Sequence 1, App1
21	326.5	19.1	376	3 US-08-458-834-1	Sequence 1, App1
22	323	18.9	1480	3 US-09-191-647-7	Sequence 7, App1
23	323	18.9	1480	3 US-09-540-245A-7	Sequence 7, App1
24	323	18.9	1480	3 US-09-540-153-7	Sequence 7, App1
25	323	18.9	1480	5 PCT-US91-09055-2	Sequence 2, App1
26	321	18.7	1480	4 US-09-182-024A-5	Sequence 5, App1
27	321	18.7	1529	4 US-09-312-283C-396	Sequence 396, App

28	320	18.7	1523	4 US-09-182-024A-2	Sequence 2, App1
29	317	18.5	1525	3 US-09-191-647-2	Sequence 2, App1
30	317	18.5	1525	3 US-09-540-245A-2	Sequence 2, App1
31	317	18.5	1525	3 US-09-540-153-2	Sequence 2, App1
32	314.5	18.4	375	1 US-08-303-238-2	Sequence 2, App1
33	314.5	18.4	375	1 US-08-458-834-2	Sequence 2, App1
34	303.5	17.7	653	4 US-09-996-243-229	Sequence 229, App
35	302	17.6	640	4 US-09-996-243-501	Sequence 501, App
36	295.5	17.3	907	4 US-09-170-496D-264	Sequence 264, App
37	295.5	17.3	907	4 US-09-170-496D-278	Sequence 278, App
38	291	17.0	1091	3 US-08-986-485-5	Sequence 5, App1
39	281.5	16.4	302	1 US-08-482-273-105	Sequence 105, App
40	280	16.3	55	1 US-08-442-063A-57	Sequence 57, App1
41	278	16.2	1101	3 US-08-986-485-2	Sequence 2, App1
42	273	15.9	605	1 US-08-190-802A-49	Sequence 49, App1
43	273	15.9	605	3 US-09-063-950-5	Sequence 5, App1
44	273	15.9	605	3 US-08-477-346-49	Sequence 49, App1
45	273	15.9	605	4 US-08-473-089-49	Sequence 49, App1

ALIGNMENTS

RESULT 1
US-08-442-063A-27
Sequence 27, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MILLER, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITILE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-27
Query Match 99.8%; Score 1709; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.6e-158;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDPEFSLGVPVCFRCQCHLRVVOCSDLGLDKVPKOLPDDTLLDLONN 61
DB 4 EASGIGPEVDDDDPEFSLGVPVCFRCQCHLRVVOCSDLGLDKVPKOLPDDTLLDLONN 63
QY 62 KITEIKDGPKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKEPKNPKT 121
DB 64 KITEIKDGPKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKEPKNPKT 123
QY 122 LOELRAHENEITKRVKVTENGLOMIVIELGTNPLKSSGIENGAFOGKKLSYIRIADTN 181
DB 124 LOELRAHENEITKRVKVTENGLOMIVIELGTNPLKSSGIENGAFOGKKLSYIRIADTN 183
QY 182 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 241
DB 184 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 243
QY 242 RELHLDNNKLTFRVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 301
DB 244 RELHLDNNKLTFRVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 303
QY 302 NPVOYWEIOPSTFRVCYVRSALQGNKY 329
DB 304 NPVOYWEIOPSTFRVCYVRSALQGNKY 331

RESULT 2
US-08-303-238-4
Sequence 4, Application US/08303238
Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-303-238-4

Query Match 99.8%; Score 1709; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 5,2e-158;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDPEFSLGVPVCFRCQCHLRVVOCSDLGLDKVPKOLPDDTLLDLONN 61
DB 32 EASGIGPEVDDDDPEFSLGVPVCFRCQCHLRVVOCSDLGLDKVPKOLPDDTLLDLONN 91
QY 62 KITEIKDGPKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKEPKNPKT 121
DB 92 KITEIKDGPKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKEPKNPKT 151
QY 122 LOELRAHENEITKRVKVTENGLOMIVIELGTNPLKSSGIENGAFOGKKLSYIRIADTN 181
DB 152 LOELRAHENEITKRVKVTENGLOMIVIELGTNPLKSSGIENGAFOGKKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 271
QY 242 RELHLDNNKLTFRVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 301
DB 272 RELHLDNNKLTFRVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 331
QY 302 NPVOYWEIOPSTFRVCYVRSALQGNKY 329
DB 332 NPVOYWEIOPSTFRVCYVRSALQGNKY 359

RESULT 3
US-08-458-834-4
Sequence 4, Application US/08458834
Patent No. 627812
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-4

Query Match 99.8%; Score 1709; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 5.2e-158;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGPVCPQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 61
DB 32 EASGIGPEVDDRDPEPSIGPVCPQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 91
QY 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKELPERKMPKT 121
DB 92 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKELPERKMPKT 151
QY 122 LOELRAHENEITKRVKVTENGNGLMIVIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 181
DB 152 LOELRAHENEITKRVKVTENGNGLMIVIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKLGSPNSISAVDNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKLGSPNSISAVDNGSLANTPHL 271
QY 242 RELHLDNNKLTFRVPGSLAEHKYIQVYVYLLHNNNISVVGSSDFCPGHNTKASYSVSLPS 301
DB 272 RELHLDNNKLTFRVPGSLAEHKYIQVYVYLLHNNNISVVGSSDFCPGHNTKASYSVSLPS 331
QY 302 NPQYWEIQSTFRVCYVRSALQLGNYK 329
DB 332 NPQYWEIQSTFRVCYVRSALQLGNYK 359

RESULT 4

US-08-272-919-2

Sequence 2, Application US/08272919

Patent No. 5567807

GENERAL INFORMATION:

APPLICANT: Craig, William S.

APPLICANT: Harper, John R.

APPLICANT: Hernandez, Sam D.

APPLICANT: Koestel, Paul J.

APPLICANT: Parker, Jonathan R.

APPLICANT: Vedvick, Thomas S.

TITLE OF INVENTION: Processes for the Purification of Human

TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/272,919

FILING DATE: 08-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 1040

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-272-919-2

Query Match 99.5%; Score 1704; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGPVCPQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 61
DB 16 EASGIGPEVDDRDPEPSIGPVCPQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 75
QY 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKELPERKMPKT 121
DB 76 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNOLKELPERKMPKT 135
QY 122 LOELRAHENEITKRVKVTENGNGLMIVIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 181
DB 136 LOELRAHENEITKRVKVTENGNGLMIVIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 195
QY 182 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKLGSPNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKLGSPNSISAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTFRVPGSLAEHKYIQVYVYLLHNNNISVVGSSDFCPGHNTKASYSVSLPS 301
DB 256 RELHLDNNKLTFRVPGSLAEHKYIQVYVYLLHNNNISVVGSSDFCPGHNTKASYSVSLPS 315
QY 302 NPQYWEIQSTFRVCYVRSALQLGNYK 328
DB 316 NPQYWEIQSTFRVCYVRSALQLGNYK 342

RESULT 5

US-08-619-916-2

Sequence 2, Application US/08619916

Patent No. 5763276

GENERAL INFORMATION:

APPLICANT: Craig, William S.

APPLICANT: Harper, John R.

APPLICANT: Hernandez, Sam D.

APPLICANT: Koestel, Paul J.

APPLICANT: Parker, Jonathan R.

APPLICANT: Vedvick, Thomas S.

TITLE OF INVENTION: Processes for the Purification of Human

TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619,916

FILING DATE: 08-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 1040

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-619-916-2

Query Match 99.5%; Score 1704; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 61
DB 16 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 75
QY 62 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 76 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 135
QY 122 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 136 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 195
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 301
DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 315
QY 302 NPVOYWEIOPSTFCVYVRSALQIGANY 328
DB 316 NPVOYWEIOPSTFCVYVRSALQIGANY 342

RESULT 6
PCT-US95-08542-2
Sequence 2, Application PC/TUS9508542
GENERAL INFORMATION:
APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium
TITLE OF INVENTION: Ions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08542
FILING DATE: 07-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Susan M.
REGISTRATION NUMBER: 36,405
REFERENCE/DOCKET NUMBER: FP-LA 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08542-2

Query Match 99.5%; Score 1704; DB 5; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 61
DB 16 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 75
QY 62 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 76 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 135
QY 122 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 136 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 195
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 301
DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 315
QY 302 NPVOYWEIOPSTFCVYVRSALQIGANY 328
DB 316 NPVOYWEIOPSTFCVYVRSALQIGANY 342

RESULT 7
5340934-4
Patent No. 5340934
APPLICANT: TERMINE, JOHN D., YOUNG, MARIAN F., FISHER, LARRY W.
ROBEY, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
SEQ ID NO: 4
LENGTH: 353
5340934-4

Query Match 96.5%; Score 1653; DB 6; Length 353;
Best Local Similarity 97.3%; Pred. No. 1.4e-152;
Matches 319; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 61
DB 26 EASGIGEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKQLPDDTLLDLDQNN 85
QY 62 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 86 KITEIKDGDPRKLNKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 145
QY 122 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 146 LOELRAHENEITKVRKVTENGINQMTIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 205
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 206 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 265
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 301
DB 266 RELHLDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVVGSSDPFCPPGHNTKKAISGVSLFS 325

Qy 302 NPVOYMEIOPSTERCYVRSATOLGNYK 329
Db 326 NPVOYMEIOPSTERCYVRSATOLGNYK 353

RESULT 8

US-08-442-063A-48
Sequence 48, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-48

Query Match 91.5%; Score 1567; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
Db 4 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 63
Qy 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPKT 121
Db 64 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPKT 123
Qy 122 LOELRAHENEITVRKVTFNGLNQMIVIELGTNPLKSSGIGENGAFQGMKKLSYIRIADTN 181
Db 124 LOELRAHENEITVRKVTFNGLNQMIVIELGTNPLKSSGIGENGAFQGMKKLSYIRIADTN 183
Qy 182 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 241
Db 184 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 243

Qy 242 RELHLDNNKLTREVGGIAEHKXIQVYILHNNNISVSGSSDPCPRGHNTKASYSVGSLSFS 301
Db 244 RELHLDNNKLTREVGGIAEHKXIQVYILHNNNISVSGSSDPCPRGHNTKASYSVGSLSFS 303
Qy 302 NP 303
Db 304 NP 305

RESULT 9

US-08-442-063A-45
Sequence 45, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-45

Query Match 83.7%; Score 1433; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.6e-131;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
Db 4 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 63
Qy 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPKT 121
Db 64 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPKT 123
Qy 122 LOELRAHENEITVRKVTFNGLNQMIVIELGTNPLKSSGIGENGAFQGMKKLSYIRIADTN 181
Db 124 LOELRAHENEITVRKVTFNGLNQMIVIELGTNPLKSSGIGENGAFQGMKKLSYIRIADTN 183
Qy 182 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 241

Db 184 ITSIPOGLPSTLTHLDGKISRVDASLKGNNLAKLGLSFNSISAVDGLANTPHL 243
QY 242 RELHLDNNKLTFRVPGGLAEHKYIOVYLIANNISVGS 279
Db 244 RELHLDNNKLTFRVPGGLAEHKYIOVYLIANNISVGS 281

RESULT 10

US-08-442-063A-42
Sequence 42, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-42

Query Match 69.2%; Score 1186; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.1e-107; Indels 0; Gaps 0;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGREVDDBRDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKDLPPDTLLDLQNN 61
Db 4 EASGIGREVDDBRDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKDLPPDTLLDLQNN 63
QY 62 KITREIDGDFKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSKNQKELPERKPKT 121
Db 64 KITREIDGDFKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSKNQKELPERKPKT 123
QY 122 LOELRAHENEITVKRYKTFENGILNOMIVIELGTNPILKSSGIENGAFOGKKLSYIRIADTN 181
Db 124 LOELRAHENEITVKRYKTFENGILNOMIVIELGTNPILKSSGIENGAFOGKKLSYIRIADTN 183
QY 182 ITSIPOGLPSTLTHLDGKISRVDASLKGNNLAKLGLSFNSISAVDN 232

Db 184 ITSIPOGLPSTLTHLDGKISRVDASLKGNNLAKLGLSFNSISAVDN 234

RESULT 11

US-08-303-238-3
Sequence 3, Application US/08303238
Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-3

Query Match 56.4%; Score 966; DB 1; Length 368;
Best Local Similarity 56.5%; Pred. No. 1e-85; Indels 2; Gaps 2;

Matches 186; Conservative 51; Mismatches 90; Indels 2; Gaps 2;

QY 2 EASGIGRE-VPDRDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKDLPPDTLLDLQNN 60
Db 40 EASGADTSGVLDPSVTPYSAMCPGCHCHLRVVOCSDLGLKSVKESIPDTLLDLQNN 99
QY 61 KITREKDDDFKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSKNQKELPERKPKT 120
Db 100 NDISELKDDFGQLQHLVLLVNNKISKIHKASPLNNVQKLYISKHNLVEIPNNLPS 159
QY 121 LOELRAHENEITVKRYKTFENGILNOMIVIELGTNPILKSSGIENGAFOGKKLSYIRIADT 180
Db 160 SLVELRIHNNRIIRKYPNGVFGSLRMNMCILEMGNPLNENGPFPGAFDGL-KANTYLRISIA 218
QY 181 NITSIPQGLPSTLTHLDGKISRVDASLKGNNLAKLGLSFNSISAVDGLANTPH 240
Db 219 KLTGIPKDLPEFTLNEIHDHNNKIOAIELEDLRYSKLYRIGLGHQOIRMIENGISFLPT 278
QY 241 LRELHLDNNKLTFRVPGGLAEHKYIOVYLIANNISVGSDDCCPGHNTKASYSGVGSF 300

Db 279 LRELHLDNNKLA RVP SGLPDLKLLQVYVYLSNNITKVGVD FCPMGFGV RAYNGISLFP 338
Qy 301 SNPVQYWEIOPSTFRCCVYRSAIQLGNKY 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNFK 367

RESULT 12

US-08-458-834-3
Sequence 3, Application US/08458834
Patent No. 6277812
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-3

Query Match 56.4%; Score 966; DB 3; Length 368;
Best Local Similarity 56.5%; Pred. No. 1e-85;

Matches 186; Conservative 51; Mismatches 90; Indels 2; Gaps 2;

Qy 2 EASGIGPE-VPDRDPEPSLGPVCFPRCOCHLRVVCSDGLDKVPKDLPPDTLLDLON 60
Db 40 EASGADTSGVLDPDSTPTYSAMCPFGCHLRVVCSDGLKSVPEISPTDTLLDLON 99
Qy 61 NKTTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERMPK 120
Db 100 NDISELRKDFKGLQHLVYLVVNNKISKIHEKAFSPLRVQKLYISKNLVEIPPLPS 159
Qy 121 TLQELRAHNEITKVRKVTENGNGMIVILGTPNPKSSGIGENARQGMKGLSYIRIADT 180
Db 160 SLVELRKHDRIRKVPNGVSGLRNNKCIEMGSPLENSGPEPAFGL-KLNYLRISIA 218
Qy 181 NITSIPQGLPSSLTEHLHLDNNKISRVDASIKGLNNLAKGLSFNSISAVDNGSLANTPH 240

Db 219 KLTGIPKDLPTLNLHLDNNKIQALEDLRLYSKLYRLGLGHNOIRMIENGSLSLFPT 278
Qy 241 LRELHLDNNKLTREVPGSLAEHKYIQVYVYLSNNISVVGSSDPEPPHNTKKSISGVSLF 300
Db 279 LRELHLDNNKLA RVP SGLPDLKLLQVYVYLSNNITKVGVD FCPMGFGV RAYNGISLFP 338
Qy 301 SNPVQYWEIOPSTFRCCVYRSAIQLGNKY 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNFK 367

RESULT 13

5340934-2
Patent No. 5340934
APPLICANT: TERKINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
APPLICANT: ROBERT, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
SEQ ID NO: 2
LENGTH: 368
5340934-2

Query Match 56.3%; Score 965; DB 6; Length 368;
Best Local Similarity 56.2%; Pred. No. 1.3e-85;

Matches 185; Conservative 53; Mismatches 89; Indels 2; Gaps 2;

Qy 2 EASGIGPE-VPDRDPEPSLGPVCFPRCOCHLRVVCSDGLDKVPKDLPPDTLLDLON 60
Db 40 EASGADTSGVLDPDSTPTYSAMCPFGCHLRVVCSDGLKSVPEISPTDTLLDLON 99
Qy 61 NKTTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERMPK 120
Db 100 NDISELRKDFKGLQHLVYLVVNNKISKIHEKAFSPLRVQKLYISKNLVEIPPLPS 159
Qy 121 TLQELRAHNEITKVRKVTENGNGMIVILGTPNPKSSGIGENARQGMKGLSYIRIADT 180
Db 160 SLVELRKHDRIRKVPNGVSGLRNNKCIEMGSPLENSGPEPAFGL-KLNYLRISIA 218
Qy 181 NITSIPQGLPSSLTEHLHLDNNKISRVDASIKGLNNLAKGLSFNSISAVDNGSLANTPH 240
Db 219 KLTGIPKDLPTLNLHLDNNKIQALEDLRLYSKLYRLGLGHNOIRMIENGSLSLFPT 278
Qy 241 LRELHLDNNKLTREVPGSLAEHKYIQVYVYLSNNISVVGSSDPEPPHNTKKSISGVSLF 300
Db 279 LRELHLDNNKLA RVP SGLPDLKLLQVYVYLSNNITKVGVD FCPMGFGV RAYNGISLFP 338
Qy 301 SNPVQYWEIOPSTFRCCVYRSAIQLGNKY 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNFK 367

RESULT 14

US-08-442-063A-39
Sequence 39, Application US/08442063A
Patent No. 5705609

GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES

Qy 301 SNPVQYWEIOPSTFRCCVYRSAIQLGNKY 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNFK 367

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-39

Query Match 55.3%; Score 948; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.1e-84;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGEVDDDDFEPSLGPVCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLDQNN 61
DB 4 EASGIGEVDDDDFEPSLGPVCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLDQNN 63
QY 62 KITRICKGDFKNTLNTALILVNNKISKVSPGAFPLVLELYLSNQKELPEKMPKT 121
DB 64 KITRICKGDFKNTLNTALILVNNKISKVSPGAFPLVLELYLSNQKELPEKMPKT 123
QY 122 LOELRAHENITKVRKTPFNGLNOMITELGTPNPLKSSGLENAGFQMKLSTYRIADTN 181
DB 124 LOELRAHENITKVRKTPFNGLNOMITELGTPNPLKSSGLENAGFQMKLSTYRIADTN 183
QY 182 ITS 184
DB 184 ITS 186

RESULT 15
US-09-724-864-43
Sequence 43, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Marison, James G.
TITLE OF INVENTION: polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 373
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-43

Query Match 54.0%; Score 925.5; DB 4; Length 373;
Best Local Similarity 53.7%; Pred. No. 9.3e-82;

Matches 173; Conservative 62; Mismatches 80; Indels 7; Gaps 2;
QY 6 IGEVDDDDFEPSLGPVCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLDQNNKITE 65
DB 56 VNPFFPPD-----LPPCPFGQCYSRVVHCSDLGLTSVNNIPDTRVVDLQNNKITE 109
QY 66 IKDDPFKNLKNLHALILVNNKISKVSPGAFPLVLELYLSNQKELPEKMPKTLOEL 125
DB 110 IKENDFKGLSLVALILNNKILKHPKTFLLTKDLRLYLSNQKELPEKMPKTLOEL 169
QY 126 RAHEENITKVRKTPFNGLNOMITELGTPNPLKSSGLENAGFQMKLSTYRIADTNIT 185
DB 170 RHDKNVKXKIQKDTFGKMNALHYLEMSANPLENNGIEPGAEGV-TVFHIRIAEAKLTSI 228
QY 186 PGLPPLSLTEIHDGKISRVDASLKGNNLAKLGSNLSAVNGSLANTPHLEH 245
DB 229 PKGLPPTLLLEHIDFKISTVELEDIKRYRELQRLDGNRRITDINGFANPVRREIH 288
QY 246 LDNNKLTFRVGGIABEKYIQVVYLIHNNNISVVGSSDFCEPGHNTKASVGLFSPNPVQ 305
DB 289 LEHNKTKKIPSGIQLKTYQIIFLHNSIAKGVNDPCFTVPKMKSLVSAISLFNNPMK 348
QY 306 YWEIQSTRCYVVRSAIQDGN 327
DB 349 YWEIQSTRCYVVRSAIQDGN 370

RESULT 16

US-08-442-063A-36
Sequence 36, Application US/08442063A
Patent No. 5705609

GENERAL INFORMATION:

APPLICANT: RIOSLAHTI, ERKKI I.
APPLICANT: PIRSCHBACHER, MICHAEL D.

APPLICANT: CARDENAS, JOSE

APPLICANT: CRAIG, WILLIAM

APPLICANT: MULLEN, DANIEL G.

TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: UNITED STATES

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/442,063A

FILING DATE: 16-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/865,652

FILING DATE: 03-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATRYN A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 1454

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-442-063A-36

Query Match 41.7%; Score 714; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 86-62;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEBSLGPVCPFRQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONN 61
DB 4 EASGIGPEVDDRDPEBSLGPVCPFRQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONN 63
QY 62 KITIEIKDGFKNLKNHALLIVNNKISKVSPGAFPLVLEKRLYLSNQKKEPEKPKPT 121
DB 64 KITIEIKDGFKNLKNHALLIVNNKISKVSPGAFPLVLEKRLYLSNQKKEPEKPKPT 123
QY 122 LOELRAHENEITKVRK 137
DB 124 LOELRAHENEITKVRK 139

RESULT 17

US-08-442-063A-33
Sequence 33, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RIOSLATTI, EKKI I.
APPLICANT: PIERSCHACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLER, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1A 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid.
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-33

Query Match 28.5%; Score 488; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 4,3e-40;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEBSLGPVCPFRQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONN 61
DB 4 EASGIGPEVDDRDPEBSLGPVCPFRQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONN 63

QY 62 KITIEIKDGFKNLKNHALLIVNNKISKVSP 92
DB 64 KITIEIKDGFKNLKNHALLIVNNKISKVSP 94

RESULT 18

US-09-188-930-305
Sequence 305, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000,1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 305.
LENGTH: 649
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-305

Query Match 19.9%; Score 341; DB 3; Length 649;
Best Local Similarity 31.6%; Pred. No. 1,6e-24;
Matches 89; Conservative 49; Mismatches 86; Indels 58; Gaps 9;

QY 24 CPERCQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONNKITIEIKDGFKNLKNHALLIV 83
DB 31 CPERCQCHLRVQCSDLGLDVKVPEKDLPTDILLDLONNKITIEIKDGFKNLKNHALLIV 81
QY 84 NNKISKVSPGAFPLVLEKRLYLSNQKKEPEKPKPTLOELRAHENEITKVRKVTENG 143
DB 82 -----LKVQRIYIYHNSLDEFPNLRKYVEHLQENNT---RTITVDSL 124
QY 144 NQNVIV---LGTNPILKSGIENGAFQGMKQSYIRIADTNTISPGSLTEHLDG 200
DB 125 SKIPLYEHLDDNSVSAVSEIEGAFRDSVYLLFLSRHLSITPGLPRTIEHLDD 184
QY 201 NKISRDASLKGILNIAKGLSPN-----SISAVNGSLA---NT 238
DB 185 NRITSSPSLHGLTSLKRLVLDGNLNNHGLDGVFNNLVNLTSLVNSSLTAAPVNL 244
QY 239 P-HIREHLDDNNKLTVPQGLAEHKYIOVV---LNNNIS 275
DB 245 PGTSLKRLYLDHNNIRVPPN--AFSTYLRQLYRLDMSNNNIS 284

RESULT 19

US-09-312-283C-305
Sequence 305, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000,1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 305
LENGTH: 649

TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-305

Query Match 19.9%; Score 341; DB 4; Length 649;
Best Local Similarity 31.6%; Pred. No. 1.6e-24;
Matches 89; Conservative 49; Mismatches 86; Indels 58; Gaps 9;

QY 24 CPEPCQCHLRVQCSDDLGVKPKDLPDPTLLDQNNKTEIKDGRKLNKLNHALLV 83
DB 31 CPVCRDAGFIYCDNRSLTSLIPVGIPEADATTLYLQNNQINN--GISPDJKN----- 81
QY 84 NNXISKVSPGAFPLVLEKLYLSKNOCKELPEKPKTLOELRAHENEITVRKTEGTL 143
DB 82 -----LTKQRIYLYNLSLDEEPTNLPKVKKSHLOENNI---RTITYDSL 124
QY 144 NQMTVIE--LGTNPLKSSGIENGAFQGMKLSYIRIADTITSIPQGLPSLTLEHLDG 200
DB 125 SKIPLLEHLDNDSVSAVSEGAFRDSNTLRLLFLSRNHLSTIPGLPRTIELRLDD 184
QY 201 NKISRVDASLKGNNLAKLGLSPV-----SIGAVDNGSLA---NT 238
DB 185 NRITISSPSLHGLTSLKRLVLDGTLNNGHGDGVFENLVNLTSLVRSSTAPVNL 244
QY 239 P--HLRELHLDNNKLTFRVGGGLAEHKYIQVY---LHNNNIS 275
DB 245 PGTSLRKLYLDQNNHINRVPPN--AFSYLKQLYRLDMNNNIS 284

RESULT 20

US-08-303-238-1
Sequence 1, Application US/08303238
Patent No. 5654270

GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITEY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-8949
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-1

Query Match 19.1%; Score 326.5; DB 1; Length 376;
Best Local Similarity 27.9%; Pred. No. 1.8e-23;
Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVDDRDPEFSPGLPVCPRQC--HLRVQCSDDLGVKPKDLPDPTLLDQNNKIT 64
DB 68 PSPDPDPD-----CPQECDCPPNPLTAMVCDNRMLKYLIP--FVPSMRKVVYFQNNQIT 118
QY 65 EIKDGRKLNKLNHALLVNKKIS--KVSPPAFPLVLEKLYLSKNOCKELPEKPKTTL 122
DB 119 SIQGVFDMNATGLMIALHGNQITSDYGRKVFSLHHLERLYLDHNNLTMPGPPLPSL 178
QY 123 QELFAHNEITKVKATVFNGINQMIIVELGTNPLKSSGIENGAFQGMKLSYIRIADNI 182
DB 179 RELHLDNQSIRVNNMLEGLENLTALYLQHDEIQEVG---SSMRGLASLILDLSTNHL 235
QY 183 TSIPOGLPSLTLEHLDGKISRVDASLKGNNLAKLGLSPNISAVDNGSLANT---P 239
DB 236 RKVDPGLPSALGQLYMEHNNVYTPDSYFRGAPKLYVRLSHNSLT--NNGLASNTFNS 293
QY 240 HIRELHLDNNKLTFRVPGGLAEHKYIQVYVLAHNNISVVGSSDFCPGHNTKASVSL 299
DB 294 SLLELDLSYNQLOKIP--PVNTMLENLYLQGNINBESSISFCTVVDVNVFSLQVYRL 350
QY 300 FSNPQYWEIOPSTFRCVYVSATQL 325
DB 351 DGNELKRSAMPADAPLCRLASLIEI 376

RESULT 21

US-08-458-834-1
Sequence 1, Application US/08458834
Patent No. 6277812

GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITEY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-1

Query Match 19.1%; Score 326.5; DB 3; Length 376;
Best Local Similarity 27.9%; Pred. No. 1.8e-23;
Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVDDRDPEPSLGPVCPFRCCQ--HLRVQCSDLGLDKVPKDPDPTTLDLQNNKIT 64
DB 68 PEPDPRD-----CPQECDCPWFPLTAMVCDNNLKLTP-FVDSRMKVFYVQNNQIT 118
QY 65 EIKDGFRLKLNHLILVNNKIS--KVSFGATPLVKLERLYLSKNQKELPEKMPKT 122
DB 119 SIQGVFNATGTLWALHGNQITSDKVGKVFSLRHLERLYLDHNNITRMGPLPRSL 178
QY 123 QELAHENITKVKATFNGLNQMIYIELGTNPLKSGIENGAFQGMKLSYRIADTN 182
DB 179 RELHLDHNOISRPNNALLEGLENTALYLQHDIEQVG--SSMRGLRSLILDLISYHL 235
QY 183 TSIPQGLPSSLTEHLHDGKNSRVDASLKLNNLAKLGISFNSISAVDNGSLANT---P 239
DB 236 RKVPDGLPSALBGLVMEHNNVTVDPSPYFGAPKLLYVRLSHNSLT--NNGLASNTFNS 293
QY 240 HRELHLDNNKLTFRVCGLAHEKTYQVYTLANNISVSGSDPCPGHNTKASYSGLV 299
DB 294 SLLELDLSYNQLOKIP--PVNTLRLNLYLQGNRINEFSSISPTVVDVVFSLQVRL 350
QY 300 FSNPVQYMEIQPSTFRCVVRSALOL 325
DB 351 DGNELKRSAMPADAPLCRLASLIER 376

RESULT 22

US-09-191-647-7
Sequence 7, Application US/09191647
Patent No. 6046015
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kild, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: 60/081,057
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 1480
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-191-647-7

Query Match 18.9%; Score 323; DB 3; Length 1480;

Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

QY 2 EASGIEPEVDDRDPEPSLGPVCPFRCCQCHLRVQCSDLGLDKVPKDPDPTTLDLQNN 61
DB 277 KCSGLTEHAPMEGAGENS-----CPHRCADGIVDCREKSLTSVPYTLPPDITDVALQNN 332
QY 62 KITKIDGDFKLNKLNHALILVNNKISKVSPGAFPLVKERLYLSKNQKELPEKMPKT 121
DB 333 FITELPKSFSSFRRLRIDLSNNNISRIADHLSGLKQLTTLVLYGNKIKDLPQGVFGK 392

QY 122 LOELR---AHENETKRVKTFNGLNQMIYIELGTNPLKSGIENGAFQGMKLSYRIAL 178
DB 393 LGSRLRLNANNEISICIRDAFRDLSLSLSDYNNIOS--LANGTFAMKSMKTVHLA 450
QY 179 -----DTN----- 181
DB 451 KNPFICDCNLRWLADYLAHKNPIETSGARCESPRMRRRIEISIREKFKCSWGLRMKLS 510
QY 182 -----ITSIPQGLPSSLTEHLHDGKNSRVDASLKG-L 214
DB 511 GECRMDSDCPAMCHCEGTTVDCTGRRRLKEIPDIPATTELLINDNEIGRISSDGLPGL 570
QY 215 NNILAKLGISFNSISAVDNGSLANTPHLREHLHDNNKLTFRVPGG--LAHEKTYQVYTLANN 272
DB 571 PHVYKLELRNQLTGIEHPAFEGASHIQELQGENKIKISNMPLGLHQ-LKTLNLYDN 629
QY 273 NISVGSSDPCPGHNTKASYSGLVFSNP 303
DB 630 QISCV-----MGSFEHLNLSLTSNLASNP 654

RESULT 23

US-09-540-245A-7
Sequence 7, Application US/09540245A
Patent No. 6270984
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kild, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 1480
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-540-245A-7

Query Match 18.9%; Score 323; DB 3; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

QY 2 EASGIEPEVDDRDPEPSLGPVCPFRCCQCHLRVQCSDLGLDKVPKDPDPTTLDLQNN 61
DB 277 KCSGLTEHAPMEGAGENS-----CPHRCADGIVDCREKSLTSVPYTLPPDITDVALQNN 332
QY 62 KITKIDGDFKLNKLNHALILVNNKISKVSPGAFPLVKERLYLSKNQKELPEKMPKT 121
DB 333 FITELPKSFSSFRRLRIDLSNNNISRIADHLSGLKQLTTLVLYGNKIKDLPQGVFGK 392
QY 122 LOELR---AHENETKRVKTFNGLNQMIYIELGTNPLKSGIENGAFQGMKLSYRIAL 178
DB 393 LGSRLRLNANNEISICIRDAFRDLSLSLSDYNNIOS--LANGTFAMKSMKTVHLA 450
QY 179 -----DTN----- 181
DB 451 KNPFICDCNLRWLADYLAHKNPIETSGARCESPRMRRRIEISIREKFKCSWGLRMKLS 510
QY 182 -----ITSIPQGLPSSLTEHLHDGKNSRVDASLKG-L 214
DB 511 GECRMDSDCPAMCHCEGTTVDCTGRRRLKEIPDIPATTELLINDNEIGRISSDGLPGL 570
QY 215 NNILAKLGISFNSISAVDNGSLANTPHLREHLHDNNKLTFRVPGG--LAHEKTYQVYTLANN 272

Db 571 PHVLKELKKNQLTGIEPNNAFEGASHIQEQLGKNTKEISNKNFLGLHQ-LKTLNLNYDN 629
QY 273 NISVGSDDPCPPGHNTKKASYGSVSLFSNP 303
Db 630 QISCV-----MPSFELHNSLTSLNLSNP 654

RESULT 24
US-09-540-153-7
Sequence 7, Application US/09540153
Patent No. 6270995
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Teesler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 1480
TYPE: PRP
ORGANISM: Drosophila melanogaster
US-09-540-153-7

Query Match 18.9%; Score 323; DB 3; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3,2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
QY 2 BASGIGPEVDDRDPEPSLGPVCPFRQCCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
Db 277 KCSGLTEHAPMEGCAENS-----CPHPCRCADGIVDCREKSLTSVPVTLPPDITDVALLEON 332
QY 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKLEPERKPKT 121
Db 333 FTTELPPKSFSSFRRLRRIDLSNNNISRIAHALSGKQKLTLLVLYGNKIKDLPSSGVFKG 392
QY 122 LOELR---AHENETVKRVKVTNGLNQMIIVIELGTPNPLKSSGIEGNAFGQMKKLSYIRLA 178
Db 393 LGSIRLLILNANEISCIKDKAFRDLSLSLSTLNNIQS--LANTGTFAMKSKVTHLA 450
QY 179 -----DTN----- 181
Db 451 KNPFICGNCNLRLADVLHKNPDIETSGARCESPKRMHRRRIEELREKFKCSGWEELRMKLS 510
QY 182 -----ITSIPQGLPESLTELHLDGKNTKISVDAASLKG-L 214
Db 511 GECRMDSDCPAMCHCEGTVDCTGRRLEKEIPRDIPLTTELLNDNEELGRISDGLFGRL 570
QY 215 NNLAKLGLSPNSISAVDNGSLAMPHLREILNNDKLTTRVPGG--LAENKCYQVNYLANN 272
Db 571 PHVLKELKKNQLTGIEPNNAFEGASHIQEQLGKNTKEISNKNFLGLHQ-LKTLNLNYDN 629
QY 273 NISVGSDDPCPPGHNTKKASYGSVSLFSNP 303
Db 630 QISCV-----MPSFELHNSLTSLNLSNP 654

RESULT 25
PCT-US91-09055-2
Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Roberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative Research
STREET: 246 Church Street
STREET: Suite 401
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06510
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: 1 to 36
IDENTIFICATION METHOD: similarity to other signal
OTHER INFORMATION: Directs Export
NAME/KEY: Four Plank-LRR-Plank domains
LOCATION: 37 to 910
IDENTIFICATION METHOD: Array of Plank-LRR-Plank
OTHER INFORMATION: mediates adhesive events
NAME/KEY: Tandem EGF-like repeats
LOCATION: 911 to 1150
IDENTIFICATION METHOD: similarity to tandem EGF-like
OTHER INFORMATION: protein-protein interactions
NAME/KEY: 7th EGF-like repeat
LOCATION: 1353 to 1393
IDENTIFICATION METHOD: similarity to epidermal growth
OTHER INFORMATION: Involvement in receptor-ligand
NAME/KEY: Alternative splice segment
LOCATION: 1394 to 1404
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: developmentally regulated
NAME/KEY: COOH-terminal region
LOCATION: 1405 to 1480
IDENTIFICATION METHOD: experimental
PCT-US91-09055-2
Query Match 18.9%; Score 323; DB 5; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3,2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
QY 2 BASGIGPEVDDRDPEPSLGPVCPFRQCCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
Db 277 KCSGLTEHAPMEGCAENS-----CPHPCRCADGIVDCREKSLTSVPVTLPPDITDVALLEON 332
QY 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVKLERLYLSKNQKLEPERKPKT 121
Db 333 FTTELPPKSFSSFRRLRRIDLSNNNISRIAHALSGKQKLTLLVLYGNKIKDLPSSGVFKG 392
QY 122 LOELR---AHENETVKRVKVTNGLNQMIIVIELGTPNPLKSSGIEGNAFGQMKKLSYIRLA 178

Db 393 LGSRLRLNNANNEISCRKQAFRLHSLSLSDNNIQS--LANGTIDANKSMKTYTALA 450
179 -----DTN----- 181
Db 451 KNPFCIDCNLWADYLHKNPLETSGARCESPKRMHRRRIISLREKFKCSWGLRMKLS 510
Qy 182 -----ITSIPQGLPPLSTTEHLHDGDKISRDVDAASLKG-L 214
Db 511 GECRMDSDCPAMCHCEGTTVDCTGRRLKEIPRDIPLHTELLDNLGRISSDGLFGRLL 570
Qy 215 NNLAALGLSFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--LAEHKTYIQVYVLIANN 272
Db 571 PHLVLELKRQQLTIEBNAFEGASHIOELQGENKIKIISNKVFLGLHQ-LKTLNLYDN 629
Qy 273 NISVVGSSDFCPGHNTHKASYSVGLFSNP 303
Db 630 QISCY-----MPGSFELHNSLTSLNLSNP 654

RESULT 26
US-09-182-024A-5
; Sequence 5, Application US/09182024A
; Patent No. 6342370
; GENERAL INFORMATION:
; APPLICANT: Connolly, Timothy
; APPLICANT: Rajput, Bhannu
; TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
; FILE REFERENCE: 640100-271
; CURRENT APPLICATION NUMBER: US/09/182,024A
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/063,946
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/096,420
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-182-024A-5

Query Match 18.7%; Score 321; DB 4; Length 1480;
Best Local Similarity 25.3%; Pred. No. 4.9e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

Qy 2 EASGIGPEVPDRDPEBPLGVCPKCCCHLRVVOCSLGLDKYPKULPPTTLIDLQNN 61
Db 277 KCSGTEHAPMECGAENS---CPHPCACADGIVDCREKSLTSVAVTLPEDTTDLLEON 332
Qy 62 KITEKIDGDFKMLKMLHLLIVNNKISKVSGAFPLVKLERLYSKQLKELPEKMKPT 121
Db 333 FITEHPSSFSFRLRLRIDSLNNNISRIADALSGQLTTLVLYGKIKIDGSGVYKG 392
Qy 122 LQELR--AHENETIKYKRVTFNGLNQMIIVIELGTNPDKSSGIENGAFQGMKLSYIRIA 178
Db 393 LGSRLRLNNANNEISCRKQAFRLHSLSLSDNNIQS--LANGTIDANKSMKTYTALA 450
Qy 179 -----DTN----- 181
Db 451 KNPFCIDCNLWADYLHKNPLETSGARCESPKRMHRRRIISLREKFKCSWGLRMKLS 510
Qy 182 -----ITSIPQGLPPLSTTEHLHDGDKISRDVDAASLKG-L 214
Db 511 GECRMDSDCPAMCHCEGTTVDCTGRRLKEIPRDIPLHTELLDNLGRISSDGLFGRLL 570
Qy 215 NNLAALGLSFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--LAEHKTYIQVYVLIANN 272
Db 571 PHLVLELKRQQLTIEBNAFEGASHIOELQGENKIKIISNKVFLGLHQ-LKTLNLYDN 629
Qy 273 NISVVGSSDFCPGHNTHKASYSVGLFSNP 303

Db 630 QISCY-----MPGSFELHNSLTSLNLSNP 654

RESULT 27
US-09-312-283C-396
; Sequence 396, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Ormest, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-396

Query Match 18.7%; Score 321; DB 4; Length 1529;
Best Local Similarity 25.4%; Pred. No. 5.2e-22;
Matches 105; Conservative 60; Mismatches 130; Indels 118; Gaps 12;

Qy 10 VPDDRDFEPLGIP-----VCPKCCCHLRVVOCSLGLDKYPKULPPTTLIDLQNNKI 63
Db 486 IPGTEDYRSKLSGDCPADLACPEKRCCEGTTVDCSNOKNKIPDHIPQYTAELRLNNNEF 545
Qy 64 TEIK-DDDFKMLKMLHLLIVNNKISKVSGAFPLVKLERLYSKQLKELPEKMKPTL 122
Db 546 TVLEATGIFPKLLPOLRKINISNNKITDIEGAFEGASGVNEILLTSRLNVOHKMKGL 605
Qy 123 QELRA-----HENETIKYKRVTFNGLNQMIIVIELGTNP 155
Db 606 ESLKTLMLRSNRISCVGNSDFTGLSVRLSLSDNNIQTTLVAPGAFGLHSLSLNLSNP 665
Qy 156 -----LKSSGIENGAFQ-----GMKRLS 173
Db 666 FNCHCHLAWIGEMLRRIYTGNPCKPYFLAKEIPIDVAIQDFTCDGNDGNSCPLS 725
Qy 174 -----YIRIADTNITSIPQGLPPLSTTEHLHDGDKISRDVDAASLGLNNAKLG 222
Db 726 RCPSECTCLDTPVVRCSNKGKLVLPKGIPIRDTVELYLDGNOFTLV-PKELSNYKHLTLIDL 784
Qy 223 SFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--GLAEHKTYIQVYVLIANNISVVG 278
Db 785 SNNRISLTSNOSFNNMTQLTLLISYNRKLCIPRPTDGL--KSLRLSLHGDNDISVV- 840
Qy 279 SSDFCPGHNTHKASYSVGLFSNPV-----QYWEIOPSTFRK 316
Db 841 -----PAGAGDLSALSHLAIAGNPLVCCDNCNMGLSDWVSEYKE--PGIARC 886

RESULT 28
US-09-182-024A-2
; Sequence 2, Application US/09182024A
; Patent No. 6342370
; GENERAL INFORMATION:
; APPLICANT: Connolly, Timothy
; APPLICANT: Rajput, Bhannu
; TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
; FILE REFERENCE: 640100-271
; CURRENT APPLICATION NUMBER: US/09/182,024A
; PRIOR FILING DATE: 1998-10-29

```

: PRIOR APPLICATION NUMBER: 60/063,946
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/096,420
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1523
: TYPE: PRT
: ORGANISM: Homo sapiens
: OS-09-182-024A-2

```

Query Match	18.7%;	Score 320;	DB 4;	Length 1523;
-------------	--------	------------	-------	--------------

OY		23	VCPERCOCHIAVWOCSDGLDKVPNDLPRDPTLLDLONNKKTTEIK-DODFQNLKTHALI	81
Dd		504	VCEPCREEGTIVCOSCOKLVRIPIBHPEEYVTDLRLNNEVSVEATGIFKKLPPLRKIN	563
OY		82	LWNKISKVSGAFTPLVKLETRYLSKQOLKEPKMKPTIOELRA---HENEITKYAKV	138
Dd		564	LSNNKIKEYREGAFDGASVOELMTGNQLETYHGVRGRGLSKTLMLRBNLSICVSND	623
OY		139	TENGIONMIVIELGTN-----	154
Dd		624	TFAGISSVRLSLBYDNRTTTTPGAFTTVSrvHHKRPVOPLOQLPLAMLGKMLRRRI	683
OY		155	-----PLKSSGIENGAQGCKKLSS-----YIRIADPNI	182
Dd		684	VSGNPRCQKPFLKEIPIDVAIOPTCDGNEBESSCOLSPROECOTMETVVRCSNKGIL	743
OY		183	TSIPQGLPPSTTELHLIDGNKISRVAASIKLGINNLAKLGSPNSISAVDNGSIANTPHLR	242
Dd		744	RALPRGMKVDTLEYLBGNHULTAV-PRELISAIRHLITLLDLSNKSISMILTNTFSMSHTLS	802
OY		243	ELHLDNNKLTREPV---GALAHEKTYIQVVYLHNNNISVVGSSDFCCPGHNETFKASYSGVGS	298
Dd		803	TLLISYNLRCLPYVAFNGL---RSRLRVJLTHGNDISSV-----PBOSFNDLISLSHLA	853
OY		299	LFSNFV	304
Dd		854	LGTMPL	859

```

RESULT 29
US-09-191-647-2
; Sequence 2, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: human
US-09-191-647-2

```

Query Match 18.5%; Score 317; DB 3; Length 1525;
Best Local Similarity 25.7%; Pred. No. 1.3e-21;
Matches 101; Conservative 60; Mismatches 120; Indels 112; Gaps 11;

```

OY      2:  CPERCQCHLRVVGCSDLGIDKVPKDLPEBDTLLDLOKNNKITEK-DDEDFNKLNNHALL 82
Db      502 CPEKCCBEGTTCVDCSNQKLNKIPEBTPQYTAELRIANNEFVTEATGIPKYLPOLRKINF 561
OY      83  VNNKISKVSPGAFTPLVYKLERLYLSKONLKEJPEKMPKTLQELRA----- 127
Db      562 SNNKIIDIEGAFBEGASGVNIELILSNLEAVQHKMKRGLESJLKTMLRNSNRITCVGNDS 621
OY      128 -----HENEITKVRKVTNGNLNOMIVIELGTP----- 155
Db      622 FIGLSSVRLLSLYDNOITTVAPGAFDTLHSLSTLNLAMPNCNCLAMLGWMLRKRIY 681
OY      156 -----LKSSGIEGAFQ-----GMKKS-----YIRADTN 182
Db      682 TGNPRCQKPYFLKEIPIPDVALQDFCTCDGDNDNCSGPLSCPECTCLDITVRCSSKGL 741
OY      183 TSIPQGLPESLTELHLHDGNKISRVAASLKGALNNILAKLGISFNGISAVDNGSLANTEHLR 242
Db      742 KVLPKIIPRDVTELYDNGQPLV-PKLSNYYKHLTLIDLSNNKISLISLNSQSPSNMQLL 800
OY      243 ELHLDDNNKLTVP---GGLAEHKYIQVVYVLIHNNNISVYGSSDFCPEGHNTKKAISYGV 298
Db      801 TLLISTNRURCIPTPTFDGL---KSLRLLSLHGDIDISV-----PEGAFNDLSLSHLA 851
OY      299 LPSNPV-----QYMIQSTERC 316
Db      852 IGANPLPYCDONNMQLSDWVKSEYK--GGLARC 882

```

```

RESULT 30
US-09-540-245A-2
; Sequence 2, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katia
; APPLICANT: Teesler-Lavigne, Marc
; TITLE OF INVENTION: Moulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PRN
; ORGANISM: human
US-09-540-245A-2

```

Query Match	18.5%	Score 317;	DB 3;	Length 1525;
Best Local Similarity	25.7%	Pred. No. 1.3e-21;		
Matches 101; Conservative	60;	Mismatches 120;	Indels 112;	Gaps 11

```
QY      24 CFFRCOCHLAIVOCSSLDGDKVFKOLPEPTLLDLONNKITEIK-DDDFKYLKNLHALLIL   82
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      502 CPEKCEGTFTVDCNSQNKINKIPEHIPOYTAELRLINNEFTVLBATGI FKKLPOLRKINF   561
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      83 VNNKISVSAGATPLVKLERLYLSKNQKELPENMPETILOELDA-----          122
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      562 SNNKTIDIEGAFEGASGVNEILLTSNRELVQHCFKGLESITLMLRSNRITCVGANDS   621
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      128 -----HENETRYKRVTNGNLNOMIVIELGNP-----                    151
        ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      622 FIGHSVRLSLTYDNQITTVAPGADPLSHSLSTLLLANPENCNCYLAIMGEMLRKRIV   681
        ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      156 -----LKSSIENGAPQ-----GMKLGS-----YFIADPTNI    182
        ||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 09:24:09 ; Search time 24 Seconds

(without alignments)
644.658 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713
Sequence: 1 VEASGIGPEVDDRDPEPSL.....QPSTFCVYASAIQIGNYK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1709	99.8	359	1	PGS2_HUMAN
2	1587.5	92.7	360	1	P07585 homo sapien
3	1584.5	92.5	360	1	Q29193 canis fam11
4	1575.5	92.0	360	1	Q46542 equus cabal
5	1564.5	91.3	360	1	PGS2_PIG
6	1564.5	91.3	360	1	PGS2_BOVIN
7	1562.5	91.2	360	1	PGS2_PABIT
8	1415	82.6	357	1	PGS2_SHEEP
9	1403	81.9	356	1	PGS2_CHICK
10	1365.5	79.7	354	1	PGS2_COTUA
11	1331.5	77.7	354	1	PGS2_MOUSE
12	1022	59.7	368	1	PGS1_RAT
13	985.5	57.5	369	1	PGS1_XENLA
14	984.5	57.5	369	1	PGS1_RAT
15	983.5	57.4	372	1	PGS1_MOUSE
16	982.5	57.4	369	1	PGS1_HORSE
17	979	57.2	368	1	PGS1_SHEEP
18	975.5	56.9	369	1	PGS1_BOVIN
19	972.5	56.8	369	1	PGS1_BOVIN
20	943.5	55.1	379	1	PGS1_CANFA
21	925.5	54.0	373	1	ASPN_HUMAN
22	616	36.0	372	1	ASPN_MOUSE
23	403.5	23.6	377	1	PGS1_PIG
24	402.5	23.5	381	1	PRIP_RAT
25	389	22.7	699	1	PRIP_BOVIN
26	386.5	22.6	378	1	ECM2_HUMAN
27	385.5	22.5	378	1	PRIP_MOUSE
28	381	22.2	135	1	PRIP_HUMAN
29	367.5	21.5	343	1	PGS1_RABIT
30	365.5	21.3	338	1	LUM_COTUA
31	365.5	21.3	343	1	LUM_HUMAN
32	356.5	20.8	342	1	LUM_CHICK
33	353.5	20.6	338	1	LUM_BOVIN
					LUM_MOUSE

34	347.5	20.3	338	1	LUM_RAT
35	342	20.0	649	1	PLR3_HUMAN
36	332	19.4	646	1	PLR1_HUMAN
37	327	19.1	1504	1	SUIT_DROME
38	325.5	19.0	352	1	KERA_HUMAN
39	322.5	18.8	376	1	FMOD_HUMAN
40	319.5	18.7	951	1	LG84_HUMAN
41	317.5	18.5	352	1	KERA_BOVIN
42	316	18.4	353	1	KERA_CHICK
43	315	18.4	353	1	KERA_COTUA
44	314.5	18.4	375	1	FMOD_BOVIN
45	313.5	18.3	951	1	LG84_RAT

ALIGNMENTS

RESULT 1
ID PGS2_HUMAN STANDARD; PRT: 359 AA.
AC P07585; Q9P020; Q9P021; Q9Y5N6; Q9Y5N9;
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=87017013; PubMed=3484330;
RA Krusius T., Ruoslahti E.;
RT "Primary structure of an extracellular matrix proteoglycan core
RT protein deduced from cloned cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93162643; PubMed=8432527;
RA Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.;
RT "Human decorin gene: intron-exon junctions and chromosomal
RT localization.";
RL Genomics 15:161-168(1993).
RN [3]
RP SEQUENCE OF 1-70 FROM N.A.
RX MEDLINE=93162642; PubMed=8432526;
RA Danielson K.G., Fazio A., Cohen I.R., Camizazzo L., Iozzo R.V.;
RT "The human decorin gene: intron-exon organization, discovery of two
RT alternatively spliced exons in the 5' untranslated region, and
RT mapping of the gene to chromosome 12q23.";
RL Genomics 15:146-160(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
RC Ce-Szabo G., Glant T.T.;
RX "Alternative splicing of human decorin.";
RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT MET-268.
RX Rieder M.J., Armet T.Z., Garington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopfner R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [7]
 RP SEQUENCE OF 31-50.
 RX MEDLINE=90073579; PubMed=2590169;
 RA Roughley P.J., White R.J.;
 RT "Dermatan sulphate proteoglycans of human articular cartilage. The
 RT properties of dermatan sulphate proteoglycans I and II.";
 RL Biochem. J. 262:823-827 (1989).
 RN [8]
 RP SEQUENCE OF 31-49.
 RX MEDLINE=87250639; PubMed=3597437;
 RA Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;
 RT "Purification and partial characterization of small proteoglycans I
 RT and II, bone sialoproteins I and II, and osteonectin from the mineral
 RT compartment of developing human bone.";
 RL J. Biol. Chem. 262:9702-9708 (1987).
 CC -I- FUNCTION: May affect the rate of fibrils formation.
 CC -I- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -I- ALTERNATIVE PRODUCTS: Named isoforms=5;
 CC Event=Alternative splicing;
 CC Name=A;
 CC IsoId=P07585-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P07585-2; Sequence=VSP_006172;
 CC Name=C;
 CC IsoId=P07585-3; Sequence=VSP_006173;
 CC Name=D;
 CC IsoId=P07585-4; Sequence=VSP_006174;
 CC Name=E;
 CC IsoId=P07585-5; Sequence=VSP_006175, VSP_006176;
 CC -I- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin.
 CC -I- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)
 CC FAMILY. CLASS I SUBFAMILY.
 CC -I- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M14219; AAB00774.1; -;
 DR EMBL; M1131; AAA52301.1; ALT SEQ.
 DR EMBL; L01125; AAA52301.1; JOINED.
 DR EMBL; L01126; AAA52301.1; JOINED.
 DR EMBL; L01127; AAA52301.1; JOINED.
 DR EMBL; L01129; AAA52301.1; JOINED.
 DR EMBL; L01130; AAA52301.1; JOINED.
 DR EMBL; M98262; AAB60901.1; -;
 DR EMBL; AF138300; AAD44713.1; -;
 DR EMBL; AF138301; AAF61437.1; -;
 DR EMBL; AF138302; AAD44714.1; -;
 DR EMBL; AF138303; AAF61438.1; -;

DR EMBL; AF138304; AAD44715.1; -;
 DR EMBL; AF491944; AAL92176.1; -;
 DR EMBL; BC005332; AAH05322.1; -;
 DR PIR; A45016; NEHUC8.
 DR Genew; HENC:2705; DCN.
 DR MIM; 125255; -;
 DR GO; GO:0007397; P.histogenesis and organogenesis; TAS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal; Alternating splicing; Polymorphism.
 FT SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 359
 FT DOMAIN 54 67
 FT REPEAT 73 93
 FT REPEAT 94 117
 FT REPEAT 118 141
 FT REPEAT 142 162
 FT REPEAT 163 186
 FT REPEAT 187 212
 FT REPEAT 213 233
 FT REPEAT 234 257
 FT REPEAT 258 281
 FT REPEAT 282 304
 FT REPEAT 305 334
 FT REPEAT 335 359
 FT DISULFID 54 67
 FT CARBOHYD 313 346
 FT CARBOHYD 34 34
 FT CARBOHYD 211 211
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT VARSPLIC 71 179
 FT VARSPLIC 73 219
 FT VARSPLIC 109 295
 FT VARSPLIC 72 75
 FT VARSPLIC 76 359
 FT VARIANT 268 268
 FT VARIANT 273 273
 FT CONFLICT 37 37
 FT CONFLICT 45 45
 SQ SEQUENCE 359 AA; 39746 MW; FF611871A1A52DD CRC64;
 Query Match 99.8%; Score 1709; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8.5e-114; Indels 0; Gaps 0;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 BASGIGPEVPPDRDEPELGPVCPRCOCHLRVVOGCSPLGLDKVXKDLPPDTLLDLQNN 61
 DB |||||
 QY 32 BASGIGPEVPPDRDEPELGPVCPRCOCHLRVVOGCSPLGLDKVXKDLPPDTLLDLQNN 91
 DB |||||
 QY 62 KITEIKDGFKNLKNLHLLIIVNNKISVSPGAFPLVYKLRVLSKNQKELPERKMT 121
 DB |||||
 QY 92 KITEIKDGFKNLKNLHLLIIVNNKISVSPGAFPLVYKLRVLSKNQKELPERKMT 151
 DB |||||
 QY 122 LOELRAHNEITTKYKRTFNGNLQMTVIELGTPNPKSGGINGNGAQGKKLSYTIATDN 181
 DB |||||
 QY 152 LOELRAHNEITTKYKRTFNGNLQMTVIELGTPNPKSGGINGNGAQGKKLSYTIATDN 211
 DB |||||
 QY 182 ITSIFOGLPSTLHLDGNKISRVDASLGLNNLAKLGLSPNSISAVDNGSLANTPHL 241
 DB |||||

```

Db      212  ITSPGGLPSPGLTEHLHDGNKTSRDPASLNGANLALGSLFNSISAVDNGSLANTPHL 271
Qy      242  RELHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNISVVGSSDFPCPGHNTKXASYSGVSLFS 301
Db      272  RELHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNISVVGSSDFPCPGHNTKXASYSGVSLFS 331
Qy      302  NPVOYWEIOPSTFRVCVYRSALIQGNKY 329
Db      332  NPVOYWEIOPSTFRVCVYRSALIQGNKY 359

RESULT 2
PGSS_CANPA
ID_PGS2_CANPA      STANDARD;      PRT;      360 AA.
AC      Q29393;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Decorin precursor (bone proteoglycan II) (Pg-S2).
GN      DCN1C.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Glant T.T.;
RL      Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP      SEQUENCE OF 244-259 FROM N.A.
RA      Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RL      Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: May affect the rate of fibrils formation (By
CC      similarity).
CC      -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC      TGF-beta. Forms a ternary complex with MPR2 and ELN (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC      similarity).
CC      -1- PTM: The attached glycosaminoglycan chain can be either
CC      chondroitin sulfate or dermatan sulfate depending upon the tissue
CC      of origin (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC      (SLRP) FAMILY. CLASS I SUBFAMILY.
CC      -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U83141; AAB51245.1; -.
DR      EMBL; L77684; AAA98062.1; -.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000372; LRR_Nterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      Pfam; PF00560; LRR; 8.
DR      Pfam; PF01462; LRRNT; 1.
DR      SMART; SMO0369; LRR_Typ; 1.
DR      SMART; SMO0013; LRRNT; 1.
KW      Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW      Leucine-rich repeat; Signal.
FT      SIGNAL          1..16
FT      PROPEP          17..30
FT      CHAIN           31..360
FT      DOMAIN          55..68
FT      REPEAT          74..94
FT      REPEAT          95..118
FT      REPEAT          119..142
FT      REPEAT          LRR-T 1.
FT      REPEAT          LRR-T 2.

```

Query Match	Best Local Similarity	Score	DB 1;	Length	DB 2;
Matches	305; Conservative	11; Mismatches	11; Indels	3; Gaps	2
REPEAT	143	163	LRR-S 2.		
FT	168	187	LRR-T 3.		
REPEAT	184	213	LRR-T 4.		
FT	214	234	LRR-S 3.		
REPEAT	235	258	LRR-T 5.		
FT	259	282	LRR-T 6.		
REPEAT	283	305	LRR-S 4.		
FT	306	335	LRR-T 7.		
REPEAT	336	360	LRR-T 8.		
FT	360	384	BY SIMILARITY.		
DISULFID	55	68	BY SIMILARITY.		
FT	314	347	O-LINKED (GLYCOSAMINOGLYCAN) (BY		
CARBOHYD	34	34	SIMILARITY).		
FT					
CARBOHYD	212	212	N-LINKED (GLUCNAC. . .) (POTENTIAL).		
FT	263	263	N-LINKED (GLUCNAC. . .) (POTENTIAL).		
CARBOHYD	304	304	N-LINKED (GLUCNAC. . .) (POTENTIAL).		
FT					
SEQUENCE	360 AA;	39980 MM;	99BEE11A9C812906 CRC64;		
Query Match	92.7%;	Score 1587.5;	DB 1;	Length 360;	
Best Local Similarity	92.4%;	Pred. No. 3.3e-105;			
Matches	305; Conservative	11; Mismatches	11; Indels	3; Gaps	2
QY	2	EASGIGPE--VPDPRDFEPSPISGAPVCFPCQCHLRVQCSDDLGLDKVPKDLPPDTLLDQ	59		
DB	32	PSGSGEPDRAPDMDLE-LIGPVCFFPCQCHLRVQCSDDLGLDKVPKDLPPDTLLDQ	90		
QY	60	NNKITEIKDGFKNLKNHAILLVNKKISKVSPGAFPLVKLERLYLSKNQKELPEKMP	119		
DB	91	NNKITEIKDGFKNLKNHAILLVNKKISKVSPGAFPLVKLERLYLSKNQKELPEKMP	150		
QY	120	KTLOELRAHEBEITKRVKVTNGNLNOMVIELGTPPLKSSGGENAGFQMKGLSTYRIAD	179		
DB	151	KTLOELRAHEBEITKRVKRVNGNLNOMVIELGTPPLKSSGGENAGFQMKGLSTYRIAD	210		
QY	180	TNIGSIPGGLPSPITELHLIDGNKISRVAASLKLGNLNAKGLSPNSISAVDNGSLANTP	239		
DB	211	TNITITPGGLPSPITELHLIDGNKISRVAASLKLGNLNAKGLSPNSISAVDNGSLANTP	270		
QY	240	HLREHLIDNNKLTIRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAYSVGSV	299		
DB	271	HLREHLIDNNKLTIRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAYSVGSV	330		
QY	300	FSNPQVWEIOPSTFRCTYVRSATIDGNYK	329		
DB	331	FSNPQVWEIOPSTFRCTYVRSATIDGNYK	360		
RESULT 3					
PGS2_HORSE					
ID	PGS2_HORSE	STANDARD;	PRT;	360 AA.	
AC	O46542;				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Decorin Precursor (Bone proteoglycan II) (Pg-62) (Dermatan sulfate				
GN	proteoglycan II) (DS-PgII).				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
NCBI	NCBI_TaxID=9796;				
NCBI	SEQUENCE FROM N.A.				
RA	Richardson D.W., Dodge G.R.;				
RT	"Effects of interleukin-1 beta and tumor necrosis factor-alpha on the				
RT	expression of matrix related genes in cultured equine articular				
RT	chondrocytes."				
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.				
CC	-I- FUNCTION: May affect the rate of fibrils formation (By				
CC	similarity).				
CC	-I- SUBUNIT: Binds to type I and type II collagen, to fibronectin and				
CC	TGF-beta. Forms a ternary complex with MFAP2 and Eln (By				
CC	similarity).				

```

CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF038127, AAB92652.1, -.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR003372, LRR_Nterm.
DR InterPro, IPR003591, LRR_typ.
DR Pfam, PF00560, LRR; 8.
DR Pfam, PF01462, LRRNT; 1.
DR SMART, SM00013, LRRNT; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 55 68
FT DISULFID 314 347
FT CARBOHYD 34 34
FT CARBOHYD 190 190
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
SQ SEQUENCE 360 AA; 39939 MW; 2DAE97CDE16F7C45 CRC64;

Query Match 92.5%; Score 1584.5; DB 1; Length 360;
Best Local Similarity 92.1%; Pred. No. 5.4e-105;
Matches 304; Conservative 12; Mismatches 11; Indels 3; Gaps 2;

QY 2 BASGIGPE--VPDDRRFEPSSLPVCPFRQCHLRVQCGDGLDVKPKDLPDPTLLDQ 59
DB 32 BASGIGPEPRIRHVDLEP-LGPVCPFRQCHLRVQCGDGLDVKPKDLPDPTLLDQ 90
QY 60 NKKITEIKGDPEKFKNLKHALILVNNKISKVSPGAFPTVVKLERLYLSFKNOKELEPEKWP 119
DB 91 NKKITEIKGDFKFKNLKHALILVNNKISKISPGAFPTVVKLERLYLSFKNOKELEPEKWP 150
QY 120 KTLQELRAHEENITKYRKATFENGALNOMIVTELGTPNPLKSSGIEGNGAFQGMKLSYIRAD 179
DB 151 KTLQELRAHEENITKYRKAVFENGALNOMIVTELGTPNPLKSSGIEGNGAFQGMKLSYIRAD 210
QY 180 TMTSTSPQGLPSTLTHLDGKISRYDAASIKGNNLAKGLISFNSTISAVNGSLAMP 239
DB 211 TMTSTSPQGLPSTLTHLDGKISRYDAASIKGNNLAKGLISFNSTISAVNGSLAMP 270

```

```

QY 240 HIREHLDDNNKLTFRVPGGLABHKYIQVYVYHANNNISVSSDFCPGHNTKKASYGVL 299
DB 271 HIREHLDDNNKLTFRVPGGLADHKYIQVYVYHANNNISAVSNDPFCPGYNTKASISGVL 330
QY 300 FSNPVOYWEIOPSTFRCYVRSALQGNVK 329
DB 331 FSNPVOYWEIOPSTFRCYVRSALQGNVK 360

RESULT 4
PGS2 FIG STANDARD; PRT; 360 AA.
ID Q9XSD9; Q9XSH4;
AC Q9XSD9; Q9XSH4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (Pg-S2).
GN DCN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Yorkshire;
RA Stephenson S.; Schnoke M.; Vesely I.;
RT "Cloning of the porcine decorin gene.";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Long;
CC IsoId=Q9XSD9-1; Sequence=Displayed.
CC Name=Short;
CC IsoId=Q9XSD9-2; Sequence=VSP 006177;
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)
CC FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF125537, AAD33578.1, -.
DR EMBL, AF140270, AAD33862.1, -.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR003372, LRR_Nterm.
DR InterPro, IPR003591, LRR_typ.
DR Pfam, PF00560, LRR; 8.
DR Pfam, PF01462, LRRNT; 1.
DR SMART, SM00369, LRR_typ; 2.
DR SMART, SM00013, LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 1 16
FT POTENTIAL.

```

FT PROPEP 17 30 BY SIMILARITY.
 FT CHAIN 31 360 DECORIN.
 FT DOMAIN 55 68 CYS-RICH.
 FT REPEAT 74 94 LRR-S 1.
 FT REPEAT 95 118 LRR-T 1.
 FT REPEAT 119 142 LRR-T 2.
 FT REPEAT 143 163 LRR-S 2.
 FT REPEAT 164 187 LRR-T 3.
 FT REPEAT 188 213 LRR-T 4.
 FT REPEAT 214 234 LRR-S 3.
 FT REPEAT 235 258 LRR-T 5.
 FT REPEAT 259 282 LRR-T 6.
 FT REPEAT 283 305 LRR-S 4.
 FT REPEAT 306 335 LRR-T 7.
 FT REPEAT 336 360 LRR-T 8.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 314 347 O-LINKED (GLYCOSAMINOGLYCAN)
 FT CARBOHYD 34 34 (BY SIMILARITY).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 281 Missing (in isoform Short).
 FT SEQUENCE 360 AA; 39899 MW; 8573DEBDBA7509 CRC64;
 SQ
 Query Match 92.0%; Score 1575.5; DB 1; Length 360;
 Beet Local Similarity 91.2%; Pred. No. 2.3e-104;
 Matches 301; Conservative 12; Mismatches 14; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEBSLGPVCPFCQCHLRVQSGDLGLDKVVKDLPDPTLLDQ 59
 DB 32 EASGIGPEPRFVEPELEP-LGPMPDFRQCHLRVQSGDLGLDKVVKDLPDPTLLDQ 90
 QY 60 NKKITEIKDGFKNLKNLHALILVNNKISKVSPGATPLVKLERLYISNQLKEPEKMP 119
 DB 91 NKKITEIKDGFKNLKNLHTLLILNNKISKISPGAPAPLVKLERLYISNQLKEPEKMP 150
 QY 120 KTLQELRAHENETTKRKATFNGLNOMVTEIGTNPFKSSGILNGAFQMKKLSYRIND 179
 DB 151 KTLQELRAHENETTKRKAKVFNGLNOMVTEIGTNPFKSSGILNGAFQMKKLSYRIND 210
 QY 180 TMTISIPQGLPSLTETLHDGNNKISVDAASLKGILNNLKLGLSFNISAVDNGSLANTP 239
 DB 211 TMTITIPQGLPSLTETLHDGNNKISVDAASLKGILNNLKLGLSFNISAVDNGSLANTP 270
 QY 240 HURELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISVWSSDFCPGHTTKKASVGSGL 299
 DB 271 HURELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISAVGSNDPCPGYNTTKKASVGSGL 330
 QY 300 FSNPVOYWEIOPSTFRGVYRSALQGNKY 329
 DB 331 FSNPVOYWEIOPSTFRGVYRSALQGNKY 360
 RESULT 5
 PGS2_BOVIN
 ID PGS2_BOVIN STANDARD; PRT; 360 AA.
 AC P21793;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Decotin precursor (Bone proteoglycan II) (PG-S2).
 GN DCN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88133946; PubMed=3435485;
 RA Day A.A., McQuillan C.I., Termine J.D., Young M.R.;

RT "Molecular cloning and sequence analysis of the cDNA for small
 RT proteoglycan II of bovine bone."
 RL Biochem. J. 248:801-805(1987).
 RN [2]
 RP SEQUENCE OF 31-54.
 RX MEDLINE=89123388; PubMed=2914936;
 RA Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
 RA Neame P.J.;
 RT "Characterization of the dermatan sulfate proteoglycans, DS-PGI and
 RT DS-PGII, from bovine articular cartilage and skin isolated by octyl-
 RT sepharose chromatography."
 RL J. Biol. Chem. 264:2876-2884(1989).
 RN [3]
 RP INTERACTION WITH MPA2 AND ELN.
 RX MEDLINE=21683536; PubMed=11721332.
 RA Reinboth B., Hansen E., Cleary E.G., Gibson M.A.;
 RT "Molecular interactions of biglycan and decorin with elastic fiber
 RT components: biglycan forms a ternary complex with tropoelastin and
 RT microfibril-associated glycoprotein 1."
 RL J. Biol. Chem. 277:3950-3957(2002).
 CC -1- FUNCTION: May affect the rate of fibrils formation.
 CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MPA2 and ELN.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LECINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS 1 SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y00712; CAA68702.1; -.
 CC PIR: S06280; S06280.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR00372; LRR_Nterm.
 CC InterPro: IPR003591; LRR_Typ.
 CC Pfam: PF00560; LRR; 9.
 CC Pfam: PF01462; LRRNT; 1.
 CC SMART: SM00369; LRR_Typ; 2.
 CC SMART: SM00013; LRRNT; 1.
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 CC Leucine-rich repeat; Signal.
 CC SIGNAL 1 16
 FT PROPEP 17 30 POTENTIAL.
 FT CHAIN 31 360 DECORIN.
 FT DOMAIN 55 68 CYS-RICH.
 FT REPEAT 74 94 LRR-S 1.
 FT REPEAT 95 118 LRR-T 1.
 FT REPEAT 119 142 LRR-T 2.
 FT REPEAT 143 163 LRR-S 2.
 FT REPEAT 164 187 LRR-T 3.
 FT REPEAT 188 213 LRR-T 4.
 FT REPEAT 214 234 LRR-S 3.
 FT REPEAT 235 258 LRR-T 5.
 FT REPEAT 259 282 LRR-T 6.
 FT REPEAT 283 305 LRR-S 4.
 FT REPEAT 306 335 LRR-T 7.
 FT REPEAT 336 360 LRR-T 8.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 314 347 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 34 34 SIMILARITY).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ	SEQUENCE	360 AA;	39837 MW;	71E84DA2D87552C0 CRC64;
Query Match	91.3%;	Score 1564.5;	DB 1;	Length 360;
Best Local Similarity	89.7%;	Pred. No. 1.4e-103;		
Matches 296;	Conservative 19;	Mismatches 12;	Indels 3;	Gaps 2
QY	2	EASGIGPE--VPDDDFRPSLGGVPCPPRCQCHLRVYQCSGLGDKYPKDLPDDTLLDQ	59	
QY	60	NNKLTETKDGFKNLKNLHALLVNNKISKVSGAFETPLVKERLYLSKNOKELPEKMP	119	
Db	32	EASGIGPEHEPEVEIEIP-MGPVCPFRQCHLRVQCSGLGDKYPKDLPDDTLLDQ	90	
QY	120	KTQGLRAHENEITVRKVTENGMLQMTIVIELGTPPLKSSGIEGNAFOGMKLLSYIRAD	179	
Db	151	KTQGLRAHENEITVRKRSVFENGLQMTIVELGTPPLKSSGIEGNAFOGMKLLSYIRAD	210	
QY	180	TNITSIPGGLPSLTSLHLDGKKISRVDAAISLKLNNLAKGLSTNSISAVNGSLIANTP	239	
Db	211	TNITITIPGGLPSLTSLHLDGKKIRKVDAAISLKLNNLAKGLSTNSISAVNGSLIANTP	270	
QY	240	HURELHNNKLTIRPVGLAEHKYIOVYLIHNNNISVYSSGDFCPRGHNTKKAASYGVL	299	
Db	271	HURELHNNKLTAKAPGVADHKTIQVYLIHNNNISVYSSGDFCPRGHNTKKAASYGVL	330	
QY	300	FSPNPQYWEIQPSTFCRCVYRSALIGLGNK 329		
Db	331	FSPNPQYWEIQPSTFCRCVYRSALIGLGNK 360		
RESULT 6				
PGS2_RABIT	STANDARD;	PRT;	360 AA.	
ID	Q28688; Q28608;			
AC	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Decorin precursor (Bone proteoglycan II) (PG-S2).			
GN	DCN.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxId=9986;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cornea;			
RX	MEDLINE=95122319; PubMed=7822148;			
RA	Zhan Q., Burrows R., Chilton C.;			
RT	"Cloning and in situ hybridization of rabbit decorin in corneal			
RT	tissues".			
RL	Invest. Ophthalmol. Vis. Sci. 36:206-215(1995).			
RP	SEQUENCE OF 38-358 FROM N.A.			
RC	TISSUE=Cartilage;			
RA	Hering T.M., Kollar J.;			
RT	"The primary structure of rabbit chondrocyte decorin deduced from			
RT	nucleotide sequence".			
RL	Submitted (NOV-1993) to the EMBL/genbank/DBJ databases.			
CC	-1- FUNCTION: May affect the rate of fibrils formation (By			
CC	similarity).			
CC	-1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and			
CC	TGF-beta. Forms a ternary complex with MFAP2 and ELN (By			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By			
CC	similarity).			
CC	-1- PTM: The attached glycosaminoglycan chain can be either			
CC	chondroitin sulfate or dermatan sulfate depending upon the tissue			
CC	of origin (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN			
CC	(SLRP) FAMILY. CLASS I SUBFAMILY.			
CC	-1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.			

Query Match	Similarity	Score	DB	Length
Basic local	90.6%	1564.5	1	360
Matches	299	Conservative	17	Mismatches 11; Indels 3; Gaps 2
QY	2	EASGIGRE--VPDRDRPEPSLGPVCPRCOCHLRVVOCSPLGLDKVPKDPDPTTLIDLQ	59	
DB	32	EASGIGDERAPRLPDL-D-MLGPVCPRCOCHLRVVOCSPLGLDKVPKDPDPTTLIDLQ	90	
QY	60	NNKLTTEIKDGFKNLKNLHLLIVNNKISKVSFGAFTPLYLRLTYLSKQULPEKMP	119	
DB	91	NNKLTTEIKDGFKNLKNLHLLIVNNKISKISFGAFTPLYLRLTYLSKQULPEKMP	150	
QY	120	KTLQELPAHNEETTKYKATFNGLNQMTIVIELGTNPLKSGSIEENGAQGMKKLSYIRIAD	179	
DB	151	KSLOELPAHNEETTKYKVSFGNMQMTIVIELGTNPLKSGSIEENGAQGMKKLSYIRIAD	210	
QY	180	TNITSIQGLPSPSLTEHLHDKGKISRVDASLKGANNLAKLGSFNSISAVDNGSLANTP	239	
DB	211	TNITTIQGLPSPSLTEHLHDKGKIKTIDASSLKGANNLAKLGSFNDISAVDNGSLANAP	270	
QY	240	HLREHLHDKNKLTRVPGGLAEHXYIQVYLVHNNNISVVGSSDFCPGHNTTKASYSGVSL	299	
DB	271	HLREHLHDKNKLTRVPGGLADHKYIQVYLVHNNNISVVGANDFCPPTNTKASYSVSL	330	
QY	300	FSNPVOYWEIOPSTFCRCVYRSALQGNKY	329	
DB	331	FSNPVOYWEIOPSTFCRCVYRSALQGNKY	360	

RESULT 7
PGS2 SHEEP STANDARD; PRT; 360 AA.
AC PGS2 SHEEP
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Ovis aries (Sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myometrium;
RX MEDLINE=20113292; PubMed=10644528;
RA Wu W.X., Zhang Q., Uno N., Derks J.B., Nathanielsz P.W.;
RT "Characterization of decorin mRNA in pregnant intrauterine tissues of
RL the ewe and regulation by steroids";
Am. J. Physiol. 278:C199-C206(2000).
CC -1- FUNCTION: May affect the rate of fibrils formation (By
similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF125041; AAF00585.1; -.
DR HSSP; P09661; IAGN.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 55 68
BY SIMILARITY.

FT DISULFID 314 347 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT SIMILARITY).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA; 39972 MW; 0095D0DFDAB8624 CRC64;
Query Match 91.2%; Score 1562.5; DB 1; Length 360;
Best Local Similarity 89.5%; Pred. No. 1.9e-103;
Matches 298; Conservative 17; Mismatches 9; Indels 9; Gaps 3;
QY 2 EASGICP-----EVEDDDEPESLGPVCPFCQCHLRVQCSDLGLDKVPKLPPTTL 56
DB 32 EASGIGPERHFEV---ELBP-MGPVCPFRQCHLRVQCSDLGLDKVPKLPPTTL 87
QY 57 DIQNNKITEIKGDGDFKNLKNLHLLVNNKISKVSPGATPIVLERLYLSTNQLKEPE 116
DB 88 DIQNNKITEIKGDGDFKNLKNLHLLVNNKISKVSPGAFAPVLERLYLSTNQLKEPE 147
QY 117 KKPCKLQELRAHENTITVRKTFENGLOMTVIELGTPIKSGTENGAFQCKLSTYR 176
DB 148 KKPCKLQELRAHENTITVRKSVFENGLOMTVIELGTPIKSGTENGAFQCKLSTYR 207
QY 177 IADNTITSIPQGLPSLTTELHDGKISRVDASLKGNNLAKLGLSFNSISAVDNGSLA 236
DB 208 IADNTITTPQGLPSLTTELHDGKISRVDASLKGNNLAKLGLSFNSISAVDNGSLA 267
QY 237 NTPHLRELHLNNKLTTRVPGGLAEHKYIQVYLLHNNNI SVYSSDFCPGHNTKASVSG 296
DB 268 NTPHLRELHLNNKLTTRVPGGLADHKYIQVYLLHNNNISALGNSDFCPGHNTKASVSG 327
QY 297 VSLFSPVQVWEIQSTTRCYVYVSAIOLGNYK 329
DB 328 VSLFSPVQVWEIQSTTRCYVYVSAIOLGNYK 360
RESULT 8
PGS2 CHICK STANDARD; PRT; 357 AA.
AC PGS2 CHICK
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=White leghorn; TISSUE=Cornea;
RX MEDLINE=9229675; PubMed=1605630;
RA Li W., Vergnes J.-P., Cornuet P.K., Haseell J.R.;
RT "cDNA clone to chick corneal chondroitin/dermatan sulfate
RT proteoglycan reveals identity to decorin";
Arch. Biochem. Biophys. 296:190-197(1992).
CC -1- FUNCTION: May affect the rate of fibrils formation (By
similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sb-sib.ch).

DR EMBL: X63797; CAA45318.1; -
DR PIR: S24317; S24317.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR_10.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 2.
DR SMART: SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 357
FT DOMAIN 52 65
FT REPEAT 71 91
FT REPEAT 92 115
FT REPEAT 116 139
FT REPEAT 140 160
FT REPEAT 161 184
FT REPEAT 185 210
FT REPEAT 211 231
FT REPEAT 232 255
FT REPEAT 256 279
FT REPEAT 280 302
FT REPEAT 303 332
FT REPEAT 333 357
FT DISULFID 52 65
FT DISULFID 311 344
FT CARBOHYD 34 34
FT CARBOHYD 209 209
FT CARBOHYD 260 260
SQ SEQUENCE 357 AA; 39687 MW; 31B104C7C3CD711D CRC64;

Query Match 82.6%; Score 1415; DB 1; Length 357;
Best Local Similarity 80.2%; Pred. No. 5.1e-93;
Matches 264; Conservative 28; Mismatches 37; Indels 0; Gaps 0;

QY 1 VEASGIGPEVPDRDREPSIGPYCPRCQCHLAVOCSDLGDKVKDLPPTLLDLON 60
DB 29 IEDEGSADMAPTDDVYISGFGPVCPCQCHLKVOCSDLGELRVKDLPPDTLLDLON 88
QY 61 NKITEIKDGFKNLKNLHLLIVNNKISKVSPGAFPLVLERLYLKSKQQLKELPEKMPK 120
DB 89 NKITEIKDGFKNLKNLHLLIVNNKISKVSPGAFPLVLERLYLKSKQQLKELPEKMPK 148
QY 121 TLQELRAHNEITKVKATVPNGLNQMIIVLELGNPLKSSGIENGAFQGMKQLSYIRADT 180
DB 149 SLQELRAHNEITKVKATVPNGLNQMIIVLELGNPLKSSGIENGAFQGMKQLSYIRADT 208
QY 181 NTSISIQGLPPSLTEHLIDGNKISRVDASIKGLNLANLKLGFNSISAVDNGSLANTH 240
DB 209 NTSISIQGLPPSLTEHLIDGNKISRVDASIKGLNLANLKLGFNSISAVDNGSLANTH 268
QY 241 LRELHLDNNKLRVPQGLAEHKYIQVYVLLHNNNISVVGSSDFCPGPHNTKASYSVSLF 300
DB 269 LRELHLDNNKLRVPQGLAEHKYIQVYVLLHNNNISVVGSSDFCPGPHNTKASYSVSLF 328
QY 301 SNPVQYWEIQSTFRCVYVRSALQLGANYK 329
DB 329 SNPVQYWEIQSTFRCVYVRSALQLGANYK 357

RESULT 9
PGS2_COTJA

ID PGS2_COTJA STANDARD; PRT; 356 AA.
AC Q9DE68;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DGN.
OS *Coturnix coturnix japonica* (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC *Coturnix*.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea, and Sclera;
RX MEDLINE=20556471; PubMed=11102759;
RA Corpeuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;
RT "Molecular cloning and relative tissue expression of decorin and
RT lumican in embryonic quail cornea."
RL Matrix Biol. 19:699-704(2000).
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MAP2 and ELN (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sb-sib.ch).

DR EMBL: AF125250; AAG48154.1; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR_10.
DR SMART: SM00369; LRR_Typ; 1.
DR SMART: SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 15
FT PROPEP 16 29
FT CHAIN 30 356
FT DOMAIN 51 64
FT REPEAT 70 90
FT REPEAT 91 114
FT REPEAT 115 138
FT REPEAT 139 159
FT REPEAT 160 183
FT REPEAT 184 209
FT REPEAT 210 230
FT REPEAT 231 254
FT REPEAT 255 278
FT REPEAT 279 301
FT REPEAT 302 331
FT REPEAT 332 356
FT DISULFID 51 64
FT DISULFID 310 343
FT CARBOHYD 33 33
FT CARBOHYD 208 208

O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 356 AA; 39571 MW; BE9583C6AED7DB26 CRC64;
 Query Match 81.9%; Score 1403; DB 1; Length 356;
 Best Local Similarity 84.1%; Pred. No. 3.6e-92;
 Matches 260; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 21 GAVCPFRCCCHLAVVQCSDLGDKVPKDLPPTTLDDLNKKITTEIKDGFKNLKNLHLL 80
 DB 48 GAVCPFRCCCHLAVVQCSDLGDKVPKDLPPTTLDDLNKKITTEIKDGFKNLKNLHLL 107
 QY 81 ILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKETLOELRAHNEKITKVKATF 140
 DB 108 ILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKETLOELRAHNEKITKVKATF 167
 QY 141 NGLNOMIVIELGTPNPKSSGIEGAGQMKKLSYRIADNTITSIQSPSTIEHLHG 200
 DB 168 NGLNOMIVIELGTPNPKSSGIEGAGQMKKLSYRIADNTITSIQSPSTIEHLHG 227
 QY 201 NKISRVDASLKLNNLAKLGLSPNSISAVDNGSLANTPHIRELHDKNKLRVPGSLAE 260
 DB 228 NKISRVDASLKLNNLAKLGLSPNSISAVDNGSLANTPHIRELHDKNKLRVPGSLAE 287
 QY 261 HKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLPSNVOYWEIOPSTFRCVYR 320
 DB 288 HKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLPSNVOYWEIOPSTFRCVYR 347
 QY 321 SAIQGNKYK 329
 DB 348 SAQVIGNYK 356

RESULT 10
 PG22 MOUSE STANDARD; PRT; 354 AA.
 ID PG22 MOUSE STANDARD; PRT; 354 AA.
 AC P28654;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Decortin precursor (Bone proteoglycan II) (PG-S2) (PG40).
 GN DCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
 RA Naitoh Y, Suzuki S;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95050610; PubMed=7961765;
 RA Scholzen T, Solureh M, Suzuki S, Reiter R, Morgan J.L.,
 RA Buchberg A.M., Stracusa L.D., Iozzo R.V.;
 RT "The murine decortin. Complete cDNA cloning, genomic organization,
 RT chromosomal assignment, and expression during organogenesis and
 RT tissue differentiation.";
 RL J. Biol. Chem. 269:28270-28281(1994).
 CC -1- FUNCTION: May affect the rate of fibrils formation.
 CC -1- SUBUNIT: Bands to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MMP2 and ELM (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X53929; CAA37876.1;
 DR PIR: A55454; A55454.
 DR HSP: P23945; 1XUN.
 DR MGI: MGI:94872; Dcn.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR00372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR; 9.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SM00369; LRR_Typ; 2.
 DR SMART: SM00013; LRRNT; 1.
 DR GlycoProtein: Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 354
 FT DOMAIN 49 62
 FT REPEAT 68 88
 FT REPEAT 89 112
 FT REPEAT 113 136
 FT REPEAT 137 157
 FT REPEAT 158 181
 FT REPEAT 182 207
 FT REPEAT 208 228
 FT REPEAT 229 252
 FT REPEAT 253 276
 FT REPEAT 277 299
 FT REPEAT 300 329
 FT REPEAT 330 354
 FT DISULFID 49 62
 FT DISULFID 308 341
 FT CARBOHYD 34 34
 FT CARBOHYD 206 206
 FT CARBOHYD 241 241
 FT CARBOHYD 257 257
 FT CARBOHYD 298 298
 SQ SEQUENCE 354 AA; 39809 MW; F05B5CC08CABF6F CRC64;

Query Match 79.7%; Score 1365.5; DB 1; Length 354;
 Best Local Similarity 79.9%; Pred. No. 1.6e-89;
 Matches 262; Conservative 28; Mismatches 33; Indels 5; Gaps 1;

QY 2 EASGIGPVPVDDRDDEPSLGPVCPFRCCCHLAVVQCSDLGDKVPKDLPPTTLDDLN 61
 DB 32 EASGIGPVPVDDRDDEPSLGPVCPFRCCCHLAVVQCSDLGDKVPKDLPPTTLDDLN 86
 QY 62 KITTEIKDGFKNLKNLHLLILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKET 121
 DB 87 KITTEIKDGFKNLKNLHLLILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKET 146
 QY 122 LOELRAHNEKITKVKATFENGQNMIVIELGTPNPKSSGIEGAGQMKKLSYRIADNT 181
 DB 147 LOELRAHNEKITKVKATFENGQNMIVIELGTPNPKSSGIEGAGQMKKLSYRIADNT 206
 QY 182 ITSIPOGLPSTIEHLHGDKNSRYDASLKLNNLAKLGLSPNSISAVDNGSLANTPH 241
 DB 207 ITAIPOGLPSTIEHLHGDKNSRYDASLKLNNLAKLGLSPNSISAVDNGSLANTPH 266
 QY 242 RELHLDNNLGLTPVPGSLAEHKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSV 301
 DB 267 RELHLDNNLGLTPVPGSLAEHKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSV 326
 QY 302 NPVOYWEIOPSTFRCVYSAIQGNKYK 329
 DB 327 NPVOYWEIOPSTFRCVYSAIQGNKYK 354

RESULT 11
PGS2 RAT STANDARD; PRT; 354 AA.

AC 001139;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-82) (PG40) (Dermatan sulfate proteoglycan-II) (DSPG).
GN DCM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=93003331; PubMed=1390895;
RA Abramson S.R., Woessner J.F.;
RT "cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).";
RL Biochim. Biophys. Acta 1132:225-227(1992).
RN [2]
RP SEQUENCE OF 11-354 FROM N.A.
RX MEDLINE=93154359; PubMed=1493796;
RA Aducci V.K., Dreher K.L.;
RT "Molecular characterization of vascular smooth muscle decorin: deduced core protein structure and regulation of gene expression.";
RL Bar. J. Cell Biol. 59:314-321(1992).
RN [3]
RP SEQUENCE OF 31-48 AND 171-191.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=89350825; PubMed=2764879;
RA Kokenyesi R., Woessner J.F.;
RT "Purification and characterization of a small dermatan sulfate proteoglycan implicated in the dilatation of the rat uterine cervix.";
RL Biochem. J. 260:413-419(1989).
CC -1- FUNCTION: May affect the rate of fibrils formation (by similarity). May be implicated in the dilatation of the rat cervix.
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- DEVELOPMENTAL STAGE: The amount of DSPG per cervix increases 4-fold during pregnancy, then falls precipitously within 1 day post partum.
CC -1- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLAS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: Z12298; CAA78170.1; -;
DR EMBL: X59859; CAA42519.1; -;
DR PIR: S29145; S29145.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR; 9.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 2.
DR SMART: SM00013; LRRNT; 1.

KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT STGNL 1 16 POTENTIAL.
FT PROPE 17 30
FT CHAIN 31 354
FT DOMAIN 49 62
FT REPEAT 68 88
FT REPEAT 89 112
FT REPEAT 113 136
FT REPEAT 137 157
FT REPEAT 158 181
FT REPEAT 182 207
FT REPEAT 208 228
FT REPEAT 229 252
FT REPEAT 253 276
FT REPEAT 277 299
FT REPEAT 300 329
FT REPEAT 330 354
FT DISULFID 49 62
FT DISULFID 308 341
FT CARBOHYD 34 34
FT CARBOHYD 184 184
FT CARBOHYD 206 206
FT CARBOHYD 241 241
FT CARBOHYD 257 257
FT CARBOHYD 298 298
SQ SEQUENCE 354 AA; 39805 MW; 152D92F42D9F5A5B CRC64;
Query Match 77.7%; Score 1331.5; DB 1; Length 354;
Best Local Similarity 77.1%; Pred. No. 4.1e-87;
Matches 253; Conservative 33; Mismatches 37; Indels 5; Gaps 1;
QY 2 BASGIGREYDDRDREPSLSGPVCFRCQCHLRVQCSDGLDLPYDLPDPTLLDLDONN 61
DB 32 BASGIGREYDDRDREPSLSGPVCFRCQCHLRVQCSDGLDLPYDLPDPTLLDLDONN 86
QY 62 KITEIKDGPDKLNKLNHAILLVNKKISKVSPGAFPLVLYLERLYSRNOLKEIPEKPKT 121
DB 87 KITEIKGAFKLNKLDHLLVLNKKISKISPEAFKVLVLERLYSRNOLKEIPEKPKT 146
QY 122 LOELRAHEMTFRVTEENGNGMNVIELGTPKSSGGENGAPQMKKLSYIRADTN 181
DB 147 LOELRAHEMTFRVTEENGNGMNVIELGTPKSSGGENGAPQMKKLSYIRADTN 206
QY 182 ITSIPQGLPPLSTELHLDGKISRVDASLKGIANLAKGLSPNSISAVDNGSIANTPHL 241
DB 207 ITAIPQGLPPLSTELHLDGKISRVDASLKGIANLAKGLSPNSISAVDNGSIANTPHL 266
QY 242 RELHLDNNKLTTRVPGLAHEKTYQVYLLHNNISVVGSSDFCPGHNTKKAASYGLPS 301
DB 267 RELHLDNNKLTTRVPGLAHEKTYQVYLLHNNISVVGSSDFCPGHNTKKAASYGLPS 326
QY 302 NPQVWEIOPTFRCYVRSATQIGNYK 329
DB 327 NPQVWEIOPTFRCYVRSATQIGNYK 354
RESULT 12
PGS1 XENLA STANDARD; PRT; 368 AA.
AC Q9IB75;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biglycan precursor.
GN BGN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Goto T., Kubota H.Y.;
 RT "cdna of biglycan of Xenopus laevis";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC
 CC -1- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB037269; BAA90246.1; -
 DR InterPro: IPR001611; LRR_Nterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01462; LRRNT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00013; LRRNT_1.
 KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 ?
 FT CHAIN 368
 FT DOMAIN 63 76
 FT REPEAT 82 102
 FT REPEAT 103 126
 FT REPEAT 127 150
 FT REPEAT 151 171
 FT REPEAT 172 195
 FT REPEAT 196 220
 FT REPEAT 221 241
 FT REPEAT 242 265
 FT REPEAT 266 289
 FT REPEAT 290 312
 FT REPEAT 313 342
 FT REPEAT 343 368
 FT DISULFID 63 76
 FT DISULFID 321 354
 SQ SEQUENCE 368 AA; 41197 MW; 53ADF7E7E3BDC528 CRC64;
 Query Match 59.7%; Score 1022; DB 1; Length 368;
 Best Local Similarity 58.8%; Pred. No. 3.3e-65;
 Matches 194; Conservative 56; Mismatches 74; Indels 4; Gaps 3;
 QY 2 EASGIGPEVDDDBFESLGP--VCFPRCCHLRVVOCSLGLDKVVKDLPPTTLDDQ 59
 DB 40 EASGVGP-IPTESIPDVLPRMDLCPGCGCHLRVVOCSLGLSLIPKLPKOTLLDDQ 98
 QY 60 NKKITIKGDGPKNLKNLHLLVNNKISVSPGAPPLVLEKLYISKQKLEPKMP 119
 DB 99 NKKITIKGDGPKNLKNLHLLVNNKISVSPGAPPLVLEKLYISKQKLEPKMP 158
 QY 120 KTLQELRAHENEITTKYKVTFNGLNOMIVIELGNPKLKSIGENGAQCKKLSYRIAD 179
 DB 159 KSLVEIRIHNENKIKKPKGVPSGLKNNNCIEMGNPLENGSIGEGADGL-KNTYLVSE 217
 QY 180 TNTSTIPQGLPSSTIELHLDGNKISRVDASLKLNNIATLGLSFNSISAVDNGSLANTP 239
 DB 218 AKLSGIPKGLPSTINELHLDNNKIQALEKEDLSQYALVYLGLGHNHIRMIEENGSLFMP 277
 QY 240 HLEHLHLDNNKLTREVPGGLAHBKTYQVYVYHNNNISVVGSSDFPCPHANTKKASVGSVL 299
 DB 278 VLREIHLHLDNNKLTREVPGGLAHBKTYQVYVYHNNNISVVGSSDFPCPHANTKKASVGSVL 337

QY 300 FSNPVQYWEIOPTFCVYVRSALDGNK 329
 DB 338 FNNPVYWEVQPATFRCTVDRLALQGNR 367
 RESULT 13
 PGSI RAT STANDARD; PRT; 369 AA.
 ID PGSI RAT
 AC P47853;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vascular smooth muscle;
 RX MEDLINE=91184222; PubMed=2081545;
 RA Dreher K.L., Asundi V.K., Matzura D., Cowan K.;
 RT "Vascular smooth muscle biglycan represents a highly conserved
 RT proteoglycan within the arterial wall."
 RL Eur. J. Cell Biol. 53:296-304(1990).
 CC -1- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, especially
 CC in articular cartilages.
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U17834; AA58797.1; -
 DR PIR: S32793; S32793.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR_9.
 DR Pfam: PF01462; LRRNT_1.
 DR SMART: SM00013; LRRNT_1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KM Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 368
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 FT REPEAT 291 313

```

FT REPEAT 314 343 LRR-T 7.
FT REPEAT 344 369 LRR-T 8.
FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 64 77 BY SIMILARITY.
FT DISULFID 322 355 BY SIMILARITY.
SQ SEQUENCE 369 AA; 41706 MM; 319DC15117PC604 CRC64;

Query Match 57.5%; Score 985.5; DB 1; Length 369;
Best Local Similarity 57.6%; Pred. No. 1.2e-62;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDRDPEPSLGPVCPFCQCHLHVOCSDLGDKVPRDLPPTLLDQ 59
DB 40 EASGSDTTSVGVDDSLTPFSAMCPFCQCHLHVOCSDLGDKVPRDLPPTLLDQ 99
QY 60 NNKTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMP 119
DB 100 NNDISELRKDFKGLQHLVYLVNNKISKHEKAFPLRLQKLYISKHNLVLEPNNLP 159
QY 120 KTLQELFAHENEITKRVKTPNGNOMVITELGNPLKSGSIEGAFQMGKLSYRIAD 179
DB 160 SSIVLELHIDNRIRKVPKGVSGIRNNMCLEMGNPLENSGFEPGARDGL-KLANYLRIS 218
QY 180 TINTISFQGLPPLSTLEHLIDGNKISRVDASLKGANLAKGLSFNSISAVNGSLANTP 239
DB 219 AKLTGIRKQDPELTNEHLIDGNKIQALEDLARYSLYRIGLGHNOIRMIENSLSFLP 278
QY 240 HLRHLIDNNKLTVPGLAEHKYIQVYVYLNNNISVVGSDFCPCPHNTRKASYSVSL 299
DB 279 TLREHLIDNNKLSHRVAGLPLDKLQVYVYLSNNITKVGINDFCPMGFGVAVYNGISL 336
QY 300 FSNPVQWEIOPSTFRCTVYVSAIQOLGNK 329
DB 339 FNNVPVWEVQPAFRCTVRLAQFNK 368

RESULT 14
PGSL_MOUSE STANDARD; PRT; 369 AA.
AC P28653; Q61355;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
GN BGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH Swiss; TISSUE=Fibroblast;
RA Naitoh Y., Suzuki S.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NH Swiss; TISSUE=Embryo;
RX MEDLINE=94319093; PubMed=8043960;
RA Rau W., Just W., Vetter U., Vogel W.;
RT "A dinucleotide repeat in the mouse biglycan gene (BST) on the X
RT chromosome".
RL Mamm. Genome 5:395-396(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast, and Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

```

```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toohyuk S., Carantini P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywnski M.I., Skalska U., Smalhus D.E.,
RA Schnerf A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 11-152 FROM N.A.
RP STRAIN=C57BL/6;
RX MEDLINE=21210929; PubMed=11311118;
RA Saenaeenen A.-M.K., Salminen H.J., Kantakokko A.J., Heinegaard D.,
RA Vuorio E.I.;
RT "Murine fibromodulin: cDNA and genomic structure, and age-related
RT expression and distribution in the knee joint."
RL Biochem. J. 355:577-585(2001).
CC -1- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -1- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X53928; CAA37875.1; -
DR EMBL; L20276; AAA64360.1; -
DR EMBL; BC005452; AAH05452.1; -
DR EMBL; BC019502; AAH19502.1; -
DR EMBL; Y11758; CAA72422.1; -
DR PIR; S20811; S20811.
DR MGD; MGI:88158; Bgn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 9
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 1 37
FT CHAIN 38 369
FT DOMAIN 64 77 BIGLYCAN.
FT REPEAT 83 103 CYS-RICH.
FT REPEAT 104 127 LRR-S 1.
FT REPEAT 128 151 LRR-T 1.
FT REPEAT 152 172 LRR-S 2.
FT REPEAT 173 196 LRR-T 3.
FT REPEAT 197 221 LRR-T 4.
FT REPEAT 222 242 LRR-S 3.

```

CC	-1-	SUBUNIT:	Forms a ternary complex with MPAP2 and ELN (By similarity).
CC	-1-	SUBCELLULAR LOCATION:	Secreted; extracellular matrix (By similarity).
CC	-1-	PM:	The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).
CC	-1-	SIMILARITY:	BELONGS TO THE SMALL LECITINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.
CC	-1-	SIMILARITY:	Contains 12 leucine-rich (LRR) repeats.
CC	-1-	SWISS-PROT entry:	is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
DR	EMBL:	AF035934;	AAB88305.1; -
DR	EMBL:	AF136020;	AAf64248.1; -
DR	InterPro:	IPIR001611;	LRR.
DR	InterPro:	IPIR000372;	LRR Nterm.
DR	InterPro:	IPIR003591;	LRR_Typ.
DR	Pfam:	PF00560;	LRR; 8.
DR	Pfam:	PF01462;	LRRNT; 1.
DR	SMART:	SM00013;	LRRNT; 1.
KW	GlycoSite:		Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
FT	SIGNAL	1	22 POTENTIAL.
FT	PROPEP	23	40 BY SIMILARITY.
FT	CHAIN	41	372 BIGLYCAN.
FT	DOMAIN	67	80 CYS-RICH.
FT	REPEAT	86	106 LRR-S 1.
FT	REPEAT	107	130 LRR-T 1.
FT	REPEAT	131	154 LRR-T 2.
FT	REPEAT	155	175 LRR-S 2.
FT	REPEAT	176	199 LRR-T 3.
FT	REPEAT	200	224 LRR-T 4.
FT	REPEAT	225	245 LRR-S 3.
FT	REPEAT	246	269 LRR-T 5.
FT	REPEAT	270	293 LRR-T 6.
FT	REPEAT	294	316 LRR-S 4.
FT	REPEAT	317	346 LRR-T 7.
FT	REPEAT	347	372 LRR-T 8.
FT	CARBOHYD	45	45 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT	CARBOHYD	51	51 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT	CARBOHYD	274	274 N-LINKED (GLUCNAc . . .) (POTENTIAL).
FT	CARBOHYD	315	315 N-LINKED (GLUCNAc . . .) (POTENTIAL).
FT	DISULFD	67	80 BY SIMILARITY.
FT	DISULFD	325	358 BY SIMILARITY.
SO	SEQUENCE	372 AA;	41924 MW; DOBBP576C5F082E CRC64;
Query Match		57.4%;	Score 983.5; DB 1; Length 372;
Best Local Similarity		57.0%;	Pred. No. 1.7e-62;
Matches 188;	Conservative	53;	Mismatches 86; Indels 3; Gaps 2
Oy	2	EASGIGB--VPDRDPSPSGVPCRCFCQCHLRVQCSDGLGVKVPDLPPDTLLDIQ	59
Dd	43	EASGADTTGGIPDDLSLTPTPSANCPFGCHCLRVQCSDGLGVKVPKISPDITLLDIQ	102
Oy	60	NNKTETIKDGDFPKJKNLHALILVNKKSKSVSPAFTPLVKLERLYLSNQOKELPEKMP	119
Dd	103	NNEISELRKDPFKLGCHLYALVLVNKKISKIHERKFSPLRLQKIYISGNHLVEIRPNLP	162
Oy	120	KTIQLERAHENEITKRKVTENGINOMIVIELGTNPILKSSGIENGAFOQMKGSLTYRIAD	179
Dd	163	SSLVELRHIDRRIRKVPKGVPSGLRNNNCMIEGMGNPLENSGFQPAGFDGL-KLVYLRISB	221
Oy	180	TNITSISIQGLPPLSELTHLDQNKSRVDAAKLGNMLAKGLSNVSISAVNGSLAMP	239
Dd	222	AKLGIKFPDLPETLNELHLDNKIQALELEDLRYSKLYRGGLGNQIRMINGSLSTFLP	281

QY 240 HURELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVSGSSDFCPGPHNTKASYSVGL 299
 DB 282 TLREHLHLDNNKLSRVPAIGLIDKLLQVYLLHNNNISVSGSSDFCPGPHNTKASYSVGL 341
 QY 300 FSNPVQWEIOPSTFCYVVRSAIOLGNK 329
 DB 342 FNNPVYWEVQATRCYTDRLAIOGNK 371

RESULT 16
 PGSL SHEEP
 ID PGSL SHEEP STANDARD; PRT; 369 AA.
 AC 046390;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Choroid plexus;
 RA Bruet L., Clements J.E.;
 Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May be involved in collagen fiber assembly. (By
 similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (by
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (by
 similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
 in articular cartilages.
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

 CC EMBL; AF034842; AAB87988.1; -.
 DR InterPro: IPR001611; LRR
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SMO0013; LRRNT; 1.
 DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 RN LRR-T 6.

FT REPEAT 291 313 LRR-S 4.
 FT REPEAT 314 343 LRR-T 7.
 FT REPEAT 344 369 LRR-T 8.
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 48 48 SIMILARITY).
 FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 271 271 SIMILARITY).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 64 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 322 355 BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41523 MW; 048C82C33909EE6 CRC64;
 Query Match 57.4%; Score 982.5; DB 1; Length 369;
 Best Local Similarity 57.3%; Pred. No. 2e-62;
 Matches 189; Conservative 51; Mismatches 87; Indels 3; Gaps 2;

QY 2 EASGIGPE--VEDDRFEPISLGPVCPFRQCHLRVQCSIDLGLDRVPKDLPPDTLLDQ 59
 DB 40 BASGAETTSGLPDLSDLPPTYSAMCPFGCHLRVQCSIDLGLKAVPKESIDTLLDQ 99
 QY 60 NKKTEIKDGPDKNLKNTLHALILVNNKISKVSPGFPLVKLEKILYSKNQKEPKRP 119
 DB 100 NNDISELRKDPKGLQHLVAVLVNNKISKIHEKAFSPLRKQKLYISKHILVEIIPNLP 159
 QY 120 KTLQELRAHENEITRYKRVTFNGLNQMTVIELGTNPPLKSSGISENGAFQGMKLSYRIAD 179
 DB 160 SSVLELRHIDNRIRVPKGVESGLNMMNCIEGNSPENSSEPGAFDGL-KNTYLRIS 218
 QY 180 TNITSIPQGLPPLSTELHLDGKNSRVDAAISLGLNLTAKGLSPNSISAVNGSLANTP 239
 DB 219 AKLTGPKDLPELTNELHLDHKKIQALEBLLRYSKLYRGLGNQRMINGSLSP 278
 QY 240 HURELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVSGSSDFCPGPHNTKASYSVGL 299
 DB 279 TLREHLHLDNNKLSRVPAIGLIDKLLQVYLLHNNNISVSGSSDFCPGPHNTKASYSVGL 338
 QY 300 FSNPVQWEIOPSTFCYVVRSAIOLGNK 329
 DB 339 FNNPVYWEVQATRCYTDRLAIOGNK 368

RESULT 17
 PGSL HUMAN
 ID PGSL HUMAN STANDARD; PRT; 368 AA.
 AC P21610; P13247;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=85174714; PubMed=2647739;
 RA Fisher L.W., Terhune J.D., Young M.F.;
 RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
 RT shows homology with proteoglycan II (decorin) and several
 RT nonconnective tissue proteins in a variety of species.";
 RL J. Biol. Chem. 264:4571-4576 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91317791; PubMed=1860845;
 RA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
 RA Terhune J.D., Young M.F.;
 RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
 RT chromosomal localization.";
 RL J. Biol. Chem. 266:14371-14377 (1991).
 RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE=20314869; PubMed=10854409;
RA Mallon A.M., Plutzer M., Bates R., Gloeckner G., Botcherby M.,
RA Nordstiek G., Strivens M.A., Kioschke P., Dangel A., Cunningham D.,
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Geyerstro J.S., Clark D., Goerdes M., Blechschmidt K.,
RA Rump A., Hinzman B., Mundy C.R., Miller W., Pousetka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.,
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man."
RL Genome Res. 10:758-775(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=22386257; PubMed=12477937;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Stauber R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mak S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rudin G.M., Hong L.,
RA Stepleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pirange C.,
RA Rata S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKeenan P.J., McKernan K.J., Malek J.A., Gunnarone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Werra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 38-57.
RX MEDLINE=90073579; PubMed=2590169;
RA Roughley P.J., White R.J.,
RT "Dermatan sulphate proteoglycans of human articular cartilage. The
RL properties of dermatan sulphate proteoglycans I and II."
RN Biochem. J. 262:823-827(1989).
RN [6]
RP SEQUENCE OF 38-66.
RX MEDLINE=87250639; PubMed=3597437;
RA Fieber L.W., Hawkins G.R., Tuxons N., Termini J.D.,
RA "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RL compartment of developing human bone."
RN J. Biol. Chem. 262:9702-9708(1987).
RN [7]
RP SEQUENCE OF 361-368 FROM N.A.
RC TISSUE=Skin.
RX MEDLINE=95187185; PubMed=7881444;
RA Junt W., Rau W., Muller R., Geertens C., Vogel W.,
RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)
RL locus."
RN Hum. Mol. Genet. 3:2268-2268(1994).
RN [8]
RP FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC [9]
RP SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC [10]
RP SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC [11]
RP TISSUE SPECIFICITY: Found in several connective tissues, especially
CC in articular cartilages.
CC [12]
RP PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC [13]
RP SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC [14]
RP SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL, J04599, AAA36009.1, -.
DR EMBL, M61553, AAA52287.1, ALT_SEQ.
DR EMBL, M61552, AAA52287.1, JOINED.
DR EMBL, U82695, -. NOT_ANNOTATED_CDS.
DR EMBL, BC002416, AAH02416.1, -.
DR EMBL, BC004244, AAH04244.1, -.
DR EMBL, U11686, AAC50117.1, -.
DR PIR, A40757, BGRUN.
DR Genew, HGNC:1044, BGN.
DR MIM, 301870, -.
DR DR GO, GO:0005578, C:extracellular matrix; NAS.
DR DR GO, GO:0005201, F:extracellular matrix structural constituent; NAS.
DR DR InterPro, IPR001611, LRR.
DR DR InterPro, IPR000372, LRR_Nterm.
DR DR InterPro, IPR003591, LRR_Typ.
DR DR Pfam, PF00560, LRR; 9.
DR DR Pfam, PF01462, LRRNT; 1.
DR DR SMART, SMO0013, LRRNT; 1.
KW Glycoprotein, Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
KT SIGNAL 1
KT PROPEP 20
KT CHAIN 37
KT DOMAIN 38
KT REPEAT 63
KT REPEAT 82
KT REPEAT 103
KT REPEAT 127
KT REPEAT 151
KT REPEAT 172
KT REPEAT 195
KT REPEAT 221
KT REPEAT 242
KT REPEAT 266
KT REPEAT 290
KT REPEAT 313
KT REPEAT 343
KT CARBOHYD 42
KT CARBOHYD 47
KT CARBOHYD 270
KT CARBOHYD 311
KT DISULFID 63
KT DISULFID 321
KT CONFLICT 139
KT CONFLICT 163
KT SEQUENCE 368
Query Match 57.2%; Score 979; DB 1; Length 368;
Beet Local Similarity 57.4%; Pred. No. 3.6e-62;
Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2.
DB 219 KLTGIPKDLPEPTLNLHDKKIKQALIEEDLRLRSKQYRGLGHNQIRMINGSLSTLPT 278

```

CC 241 LREHLHNNKLTFRPGGLAEHKKYIOVYLLNNNISVVGSSDFPCPGHNTKASYSGVSLF 300
DB 279 LREHLHNNKLTFRPGGLAEHKKYIOVYLLNNNISVVGSSDFPCPGHNTKASYSGVSLF 338
QY 301 SNPVQWEIOPSTFRCCYVRSALQOLGNK 329
DB 339 NNEVPYWEVQPATFRCTVTRIALQIFGNK 367

RESULT 18
PGS1 BOVIN STANDARD; PRT; 369 AA.

AC P21809; P79259;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1) (Leucine-rich PG I).
GN BGN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=96113563; PubMed=8673009;
RA Xu J.H., Radhakrishnamurthy B., Srinivasan S.R., Berenson G.S.;
RT "Primary structure of bovine aorta biglycan core protein deduced from cloned cDNA."
RL Biochem. Mol. Biol. Int. 37:263-272(1995).
RN [2]
RP SEQUENCE OF 38-369.
RC TISSUE=Cartilage;
RX MEDLINE=89255324; PubMed=2656687;
RA Neame P.J., Choi H.U., Rosenberg L.C.;
RT "The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage."
RL J. Biol. Chem. 264:8653-8661(1989).
RN [3]
RP SEQUENCE OF 38-63.
RC TISSUE=Cartilage;
RX MEDLINE=89123388; PubMed=2914936;
RA Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.;
RT "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl-sepharose chromatography."
RL J. Biol. Chem. 264:2876-2884(1989).
RN [4]
RP INTERACTION WITH MPA2 AND ELN.
RX MEDLINE=21683536; PubMed=1173132;
RA Reinboth B., Hansen E., Cleary E.G., Gibson M.A.;
RT "Molecular interactions of biglycan and decorin with elastic fiber components: biglycan forms a ternary complex with tropoelastin and microfibril-associated glycoprotein 1."
RL J. Biol. Chem. 277:3950-3957(2002).
CC -1- FUNCTION: May be involved in collagen fiber assembly.
CC -1- SUBUNIT: Forms a ternary complex with MPA2 and ELN.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- TISSUE SPECIFICITY: Found in several connective tissues, especially in articular cartilages.
CC -1- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate.
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; S82652; AAB46746.2; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Signal; Repeat;
KW Leucine-rich repeat.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 369
FT DOMAIN 64 77
FT REPEAT 83 103
FT REPEAT 104 127
FT REPEAT 128 151
FT REPEAT 152 172
FT REPEAT 173 196
FT REPEAT 197 221
FT REPEAT 222 242
FT REPEAT 243 266
FT REPEAT 267 290
FT REPEAT 291 313
FT REPEAT 314 343
FT CARBOHYD 42 42
FT CARBOHYD 48 48
FT CARBOHYD 271 271
FT CARBOHYD 312 312
FT DISULFID 64 77
FT DISULFID 322 355
FT CONFLICT 152 152
FT CONFLICT 188 188
FT CONFLICT 354 354
FT CONFLICT 358 359
SQ SEQUENCE 369 AA; 41509 MW; 453309PFD1B8872 CRC64;
Query Match 56.9%; Score 975.5; DB 1; Length 369;
Best Local Similarity 57.0%; Pred. No. 6.3e-62;
Matches 188; Conservative 51; Mismatches 88; Indels 3; Gaps 2;
QY 2 EASGIGPE--VDDRDFFPSIGAPVCPFRQCHLRVVGSSDGLDVRVDPDPTLLDQ 59
DB 40 EASGAEITSGIPDLDSLPPTYSAMCPFGCHLRVVGSSDGLDRAVPEISDPTLLDQ 99
QY 60 NNKITEIKDGDPRKNTKNTLALVLVNNKISKSPGAFPLVYKLERLYLSKNQKELPEKMP 119
DB 100 NNDISLRKDDPKGLQHLVAVLVNNKISKIHEKAFSPLRKIQKLYISKNHLCETIPNIP 159
QY 120 KTLQELRAHENEITVARKTFENGINQWIVIEGTNPPLKSSGIENGAFQOMKGLSTRIRAD 179
DB 160 SSVIVLRKIDNRIRKRVPGKVSGLANMNCIEGNGPLENGSGEPAPFDGL KLTAKIRISE 218
QY 180 TNITSIPQGLPSLTSLHLDGKNSRVDASLKIANTLAKLGLSFNSISAVDNGSLAMP 239
DB 219 AALTGIDPDLPTLNLHLHDHKKIQALELDLRLRSKLYRGLGHNQIRMIENGSLFLP 278
QY 240 HIREHLHNNKLTFRPGGLAEHKKYIOVYLLNNNISVVGSSDFPCPGHNTKASYSGVSL 299
DB 279 TLREHLHNNKLTFRPGGLAEHKKYIOVYLLNNNISVVGSSDFPCPGHNTKASYSGVSL 338
QY 300 FSNPVQWEIOPSTFRCCYVRSALQOLGNK 329
DB 339 NNEVPYWEVQPATFRCTVTRIALQIFGNK 368

RESULT 19
PGS1 CANFA STANDARD; PRT; 369 AA.

AC 002678;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_Taxid=9615;
 RX
 RN
 RP SEQUENCE FROM N.A.
 RA Glantz T.T.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May be involved in collagen fiber assembly. (By
 similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 similarity).
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; 083140; AAB51244.1; -.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 FT REPEAT 291 313
 FT REPEAT 314 343
 FT REPEAT 344 369
 FT CARBOHYD 42 42
 FT CARBOHYD 48 48
 FT CARBOHYD 271 271
 FT CARBOHYD 312 312
 FT DISULFID 64 77
 FT DISULFID 322 355
 FT SEQUENCE 369 AA; 41566 MW; 8C919B922D5377B6 CRC64;
 SQ
 Query Match 56.8%; Score 972.5; DB 1; Length 369;
 Best Local Similarity 57.3%; Pred. No. 1e-61;
 Matches 189; Conservative 49; Mismatches 89; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDRDEPPSLGVCPPRCQCHLRVQCSGLGDKRVPDLPPDTLLDQ 59
 DB 40 EASGAGTTSVGPDLALTPYSANCPRGCHHLKLVQCSGLGKAVPEISPDMLDQ 99
 QY 60 NNNKTEIKDGPDKLKNLHLLVNNKISKVSPGAFPLVLEKLYLSKQDLPEKMP 119
 DB 100 NNDISELRADDFKGIHLYALVLYVNNKISKIHEKAFSPRLQKLYSKNHLVEIPVLP 159
 QY 120 KTLQELRAHENEIRKRVVFENGINQWIVIELGNTPLKSSGIEKNGAFQMKLSYIRIAD 179
 DB 160 SSVLELRTHDRIRKRVPGVPSGLRNMMCIEMGSPLENSEPGPAFDGL-KNLTIRISE 218
 QY 180 TNTISIPQGLPPSTELHLDGNKISRVAASLKGNNLAKLGLSFNSISAVDNGSLANTP 239
 DB 219 AKLTGIPKDLPETNELHLDNNKIQALBELDLRSKLYRGLGHNQIRMENGSFLP 278
 QY 240 HIRELHLDNNKLTTRVPGSLAEHKYIQVYLLNNNISVTGSSDPCEPHNTKASISGVSL 299
 DB 279 TLREIHLNNKLSRPSGLPDLKLLQVYVYLTNNITKGVNDFCPVGGVKAAYNGISL 338
 QY 300 FSNPYQWEIQSPMPCYVRSATQGNKY 329
 DB 339 FNNPVWEVQPAFRCTDRLAIQPNKY 368
 RESULT 20
 ASPN HUMAN
 ID ASPN HUMAN STANDARD; PRT; 379 AA.
 AC Q9BXN1; Q96K79; Q96LD0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Asporin precursor (Periodontal ligament associated protein-1) (PLAP-1).
 GN ASPN OR PLAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITE
 RP ASN-281, MASS SPECTROMETRY, AND POLYMORPHISM OF POLY-ASP REGION.
 RC TISSUE=Cartilage;
 RX MEDLINE=21192276; PubMed=11152692;
 RA Lorenzo P., Aspborg A., Oenertford P., Bayliss M.T., Neame P.J.,
 Heinigaard D.;
 RT "Identification and characterization of asporin. A novel member of the
 leucine-rich repeat protein family closely related to decorin and
 biglycan.";
 RT J. Biol. Chem. 276:12201-12211 (2001).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21472263; PubMed=11587855;
 RA Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji T., Nakahira Y.,
 Ikezawa K., Takayama S.-I., Matsubara K., Okada H.;
 RT "Expression profile of active genes in human periodontal ligament and
 isolation of PLAP-1, a novel SLRP family gene.";
 RT Gene 275:279-286 (2001).
 RN
 RP SEQUENCE OF 1-242 FROM N.A.
 RC TISSUE=Embryo;
 RA Isegaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
 Wagaetsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
 Ninomiya K., Iwayanagi T.;
 RT "NEO human cDNA sequencing project.";
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=21192277; PubMed=11152695;

RA Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspaecher H.,
 RA Zhou W., de Crombrughe B., Hoeoek M., Mayne R.,
 RT "Expression pattern and gene characterization of asporin. A newly
 RT discovered member of the leucine-rich repeat protein family.",
 RT J. Biol. Chem. 276:12212-12221(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- TISSUE SPECIFICITY: Higher levels in osteoarthritic articular
 CC cartilage, aorta, uterus. Moderate expression in small intestine,
 CC heart, liver, bladder, ovary, stomach, and in the adrenal,
 CC thyroid, and mammary glands. Low expression in trachea, bone
 CC marrow, and lung.
 CC -1- PTM: Does not contain a serine/glycine dipeptide sequence required
 CC for the assembly of O-linked glycosaminoglycans and is probably
 CC not a proteoglycan. The N-linked glycan at Asp-281 is composed of
 CC variable structures of GlcNAc, mannose, fucose, HexNAc and hexose.
 CC -1- POLYMORPHISM: The poly-Asp region of ASPN is polymorphic and
 CC ranges at least from 11 to 17 Asp.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: AF316824; AAK5161.1; -;
 DR EMBL: AY029191; AAK31800.1; -;
 DR EMBL: AK027359; BAB5060.1; -;
 DR Genew: HGNC:14872; ASPN.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01462; LRRNT_1.
 DR SMART: SMO0013; LRRNT_1.
 DR GlycoProtein: Extracellular matrix; Signal; Repeat;
 KW leucine-rich repeat; Polymorphism; Triplet repeat expansion.
 KM
 FT SIGNAL 1 14
 FT PROPEP 15 32
 FT CHAIN 33 379
 FT DOMAIN 76 89
 FT REPEAT 95 115
 FT REPEAT 116 139
 FT REPEAT 140 163
 FT REPEAT 164 184
 FT REPEAT 185 208
 FT REPEAT 209 233
 FT REPEAT 234 254
 FT REPEAT 255 278
 FT REPEAT 279 302
 FT REPEAT 303 325
 FT REPEAT 326 355
 FT REPEAT 356 379
 FT DISULFID 332 365
 FT DOMAIN 36 52
 FT CARBOHYD 54 54
 FT CARBOHYD 281 281
 FT CONFLICT 237 242
 FT CONFLICT 237 242
 SQ SEQUENCE 379 AA; 43302 MW; 786625859E26A56D CRC64;
 Query Match 55.1%; Score 943.5; DB 1; Length 379;
 Best Local Similarity 55.0%; Pred. No. 1.2e-59;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 11 PDDRDEPSLGPVPCRCOCHLRVYVCSLDGLDKVFKDLPPTTLLDLDNNKITEKDD 70
 DB 61 PSHHPFPLFPKCPGCGCCYRSHVHSCSDGLSVTTNLPDTRMLDLDNNKITEKEND 120
 QY 71 FNNLKNLHALLVNNKISKVSFGAFTPLVETRLYSKQLKELPEKMKPTQLQELRAHNN 130

DB 121 FGLGISVGLIANNKTKIKHKAFLTTKGLARLVLSHQSLSEIPLNPKSLAEIRIHEN 180
 QY 131 EITKYRKATNGNOMIVIEIETGPNLPSKSGIENGAPQGNKLSYRIADNTITSIPQGLP 190
 DB 181 KYKKIIOKTFKGMNLAHLVLEMSANPLDNNNGIEPGAPEGV-TVFHIRIAEAKLTSYKGLP 239
 QY 191 PELTEHLIDGNKISVDAASLKLNNLAKLGISFNSISAVNDGSLANTPLHELHDNNK 250
 DB 240 FTLEHLADYNTKISTVELDEDFRYVELQRLGNNKIDIEGSLANIPRAVEIHLNNK 299
 QY 251 LTRVPGLAEHKXIOVVYLNHNNNISVGSDDPCPEGHTTKKASVGSVLSFNPVQWEIO 310
 DB 300 LKKISGLPELKYTLQIIFLHNSISARVGVNDCTVPKPKSLYSAISLFPNPKYKWEQ 359
 QY 311 PPTPRCYVYRSAIQLGNTY 328
 DB 360 PATPRCVLSRMSVQLGNF 377
 RESULT 21
 ASPN_MOUSE STANDARD; PRT; 373 AA.
 AC 099MQ4; Q9D6A2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Asporin precursor.
 GN ASPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X 129/SvJ; TISSUE=Aorta;
 RX MEDLINE=21192276; PubMed=11152692;
 RA Lorenzo P., Aspegberg A., Oemerford P., Bayliss M.T., Neame P.J.,
 RA Heinegaard D.,
 RT "Identification and characterization of asporin. A novel member of the
 RT leucine-rich repeat protein family closely related to decorin and
 RT biglycan."
 RT J. Biol. Chem. 276:12201-12211(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzaletti J., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,

ID	PREP_RAT	STANDARD;	PRT;	377 AA.
AC	Q9EQP5;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Prolagin precursor (proline-arginine-rich end leucine-rich repeat protein).			
DN	PRELP.			
OC	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=101116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Connective tissue;			
RX	MEDLINE=20576219; PubMed=11007795;			
RA	Bergstrom E., Appberg A., Heinegaard D., Sommarin Y., Spillmann D.;			
RT	"The amino-terminal part of PRELP binds to heparin and heparan sulfate.";			
RL	J. Biol. Chem. 275:40695-40702(2000).			
CC	-1- FUNCTION: May anchor basement membranes to the underlying connective tissue (By similarity).			
CC	-1- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.			
CC	-1- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.			
CC	-1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF163569; AAG23724.1; -.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000372; LRR_Nterm.			
DR	InterPro; IPR000359; LRR_typ.			
DR	Pfam; PF00560; LRR_7.			
DR	Pfam; PF01462; LRRNT; 1.			
DR	SMART; SM00013; LRRNT; 1.			
KW	Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat; Signal.			
KM				
FT	CHAIN	1	21	POTENTIAL.
FT	DOMAIN	22	377	PROLAGIN.
FT	REPEAT	68	84	CYS-RICH.
FT	REPEAT	90	109	LRR-S 1.
FT	REPEAT	110	133	LRR-T 1.
FT	REPEAT	134	157	LRR-T 2.
FT	REPEAT	158	178	LRR-S 2.
FT	REPEAT	179	202	LRR-T 3.
FT	REPEAT	203	228	LRR-T 4.
FT	REPEAT	229	249	LRR-S 3.
FT	REPEAT	250	273	LRR-T 5.
FT	REPEAT	274	298	LRR-T 6.
FT	REPEAT	299	318	LRR-S 4.
FT	REPEAT	319	357	LRR-T 7.
FT	REPEAT	358	377	LRR-T 8.
FT	DOMAIN	192	197	POLY-LBU.
FT	DISULFID	327	368	BY SIMILARITY.
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	284	284	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	322	322	N-LINKED (GLCNAC. . .) (POTENTIAL).
QO	SEQUENCE	377 AA;	43179 KM;	79CBB62534753C46 CRC64;

CC		perlecan and triple helical collagens type I and type II (By similarity).
CC	-I-	SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC	-I-	TISSUE SPECIFICITY: Expressed in cartilage throughout both fetal development and post-natal life. It is also expressed in the developing embryo prior to skeletogenesis. In adult, highest expression in lung, lower levels in cardiac and skeletal muscle.
CC	-I-	DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain (By similarity').
CC	-I-	SMILIARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.
CC	-I-	SMILIARITY: Contains 12 leucine-rich (LRR) repeats.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sdb.ch/announce or send an email to license@isb-sdb.ch).
CC		-----
DR	EMBL;	AF261888; AAF72994.2; .
DR	EMBL;	AF261887; AAF72994.2; JOINED.
DR	EMBL;	BC019775; AAH19775.1; .
DR	MED;	MGI:215110; PreIp.
DR	InterPro;	IPR001611; LRR.
DR	InterPro;	IPR000372; LRR_Nterm.
DR	InterPro;	IPR003591; LRR_Typ.
DR	Pfam;	PF00560; LRR; 7.
DR	Pfam;	PF01462; LRRT; 1.
DR	SMART;	SMO0013; LRRT; 1.
KM		Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat; Signal.
FT	CHAIN	1 21 POTENTIAL.
FT	DOMAIN	22 378 PROLARGIN.
FT	REPEAT	69 85 CYS-RICH.
FT	REPEAT	91 110 LRR-S 1.
FT	REPEAT	111 134 LRR-T 1.
FT	REPEAT	135 158 LRR-T 2.
FT	REPEAT	159 179 LRR-S 2.
FT	REPEAT	180 203 LRR-T 3.
FT	REPEAT	204 229 LRR-T 4.
FT	REPEAT	230 250 LRR-S 3.
FT	REPEAT	251 274 LRR-T 5.
FT	REPEAT	275 299 LRR-T 6.
FT	REPEAT	300 319 LRR-S 4.
FT	REPEAT	320 358 LRR-T 7.
FT	REPEAT	359 378 LRR-T 8.
FT	DOMAIN	193 198 POLY-LRU.
FT	DISULFD	328 369 BY SIMILARITY.
FT	CARBOHYD	120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	378 AA; 43292 MW; 81654FB9DF55186 CRC64;
Oy	Query Match	22.6%; Score 386.5; DB 1; Length 378;
Oy	Best Local Similarity	32.2%; Pred. No. 2; 9e-20;
Oy	Matches	93; Conservative 57; Mismatches 124; Indels 15; Gaps 6,
Dd	50 EPTDLPPLPG--PPSVFPDCPRECYCPDPFSALYCDSKRLRVVP-IPIRIHYLYL	105
Oy	59 QNNKITETKDGFKNLKIMHALILVNNNISKVSPEAFPLVLGLERTLYSKNQIKELPERM	118
Dd	106 QNNFITTELPLESFQWATGLRWNVNDNNIRKYVDQGVLGKLPSLATLVNEKQLLEVPASL	165
Oy	119 PKTLQELFAHENETITVKAKVTTFNGINOMIVIELGTNPLSKSIGENGAFQMKGSYIRIA	178
Dd	166 PRNLQQLISQNTLSIRIPGVFSKLENLLDLQHNRLSDGVFKADTEFGKLNLMQNLIA	225

Qy	173	DNMT31PQGLPEPSLTLHLTQNKTSRDPAASLKGANLALGSLFSPNISAVDNG---	SL 233
Db	226	HNILRQMPKPRVQAHQHYLVLSNKKLETPNGVFQDFPFLAIRFRNNYGLS--DRGLPQNS	283
Qy	236	ANTPHRLRLDNNKLTLPVPGGLAEHKYIQVYVYLNHNINSIVGSSDPCP	284
Db	284	FNISNLVYVHLHSNKKISNVP---ALSNNLEHLYLNHNINSIEKINGTQICP	329
RESULT 27			
PRLP_HUMAN			
ID	PRLP_HUMAN	STANDARD;	PRT; 382 AA.
AC	ps188;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Prolagin precursor (Proline-arginine-rich end leucine-rich repeat protein).		
DE	PRELP.		
GN	PRELP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RX	MEDLINE=96029653; PubMed=7552739.		
RA	Bengtsson E., Neame P.J., Heinegaard D., Sommerin Y.;		
RT	"The primary structure of a basic leucine-rich repeat protein, PRELP,		
RT	found in connective tissues.";		
RL	J. Biol. Chem. 270:25639-25644.(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97127584; PubMed=8954791;		
RA	Grover J., Chen X.-N., Korenberg J.R., Recklies A.D., Roughley P.J.;		
RT	"The gene organization, chromosome location, and expression of a		
RT	55-kDa matrix protein (PRELP) of human articular cartilage.";		
RL	Genomics 38:109-117(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas, and Spleen;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klauser R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marcusna K., Farmer A.F., Rubin G.M., Hong L.,		
RA	Stampleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Bromstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,		
RA	Raba S.S., Loggellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarate P.H.,		
RA	Richard S., Morlan K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,		
RA	Vallalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faley J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,		
RA	Schnecker A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RL	-1: FUNCTION: May anchor basement membranes to the underlying		
CC	connective tissue (By similarity).		
CC	-1: SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan		
CC	perlecan and triple helical collagens type I and type II (By		
CC	similarity).		
CC	-1: SUBCELLULAR LOCATION: Secreted; extracellular matrix.		
CC	-1: TISSUE SPECIFICITY: Connective tissue.		
CC	-1: DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and		
CC	heparan sulfate. Binds collagens type I and type II through its		
CC	leucine-rich repeat domain (By similarity).		
CC	-1: SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN		

235
283

```

CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U23089; AAC50230.1; -
CC EMBL; U41344; AAC18782.1; -
CC EMBL; U41343; AAC18782.1; JOINED.
CC EMBL; BC032498; AAH32498.1; -
CC PIR; I39068; I39068.
CC Genew; HGNC:9357; FREL.P.
CC MIM; 601914; -
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC Pfam; PF00560; LRR; 8.
CC SMART; SM00013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
CC Signal; Polymorphism.
CC SIGNAL; 1 20
CC CHAIN; 21 382
CC DOMAIN; 73 89
CC REPEAT; 95 114
CC REPEAT; 115 138
CC REPEAT; 139 162
CC REPEAT; 163 183
CC REPEAT; 184 207
CC REPEAT; 208 233
CC REPEAT; 234 254
CC REPEAT; 255 278
CC REPEAT; 279 303
CC REPEAT; 304 323
CC REPEAT; 324 362
CC REPEAT; 363 382
CC DOMAIN; 197 202
CC DISULFID; 332 373
CC CARBOHYD; 124 124
CC CARBOHYD; 289 289
CC CARBOHYD; 320 320
CC CARBOHYD; 327 327
CC VARIANT; 348 348
CC
CC SEQUENCE 382 AA; 43809 MW; A1C4E16B7515695 CRC64;
CC
CC Query Match 22.5%; Score 385.5; DB 1; Length 382;
CC Best Local Similarity 31.5%; Pred. No. 3,4e-20;
CC Matches 91; Conservative 59; Mismatches 124; Indels 15; Gaps 6;
CC
CC 2 BAAGIGPEVDDDDFEPSGLPVCPRQC--HRAVQSGDLGIDKVPKLPDPTLLDL 58
CC 54 EPTDPPPLPPG--PPSIPDCPRCEYCPDPPSALYCDSRMIRKPV-IIPRIHLYL 109
CC 59 QNKKITEIKDGFKNLKNLALILVNNKISKVSPGAFPIVYKLERLYLSKNQKELPEKM 118
CC 110 QNNPITBLPVSQNTGLKWINLNNRIRKIDQRYLEKIPGLVPLYMERNQLEVPASAL 169
CC 119 PKTLQELRAHENEITKRVKTYFNGLNQMIYIEIGTNPILKSSGIENGAFQMKLSYIRIA 178
CC 170 PRULBQRLSQNHISIRLPVGVFSKENTLILLDQHNRLSGVGRKPTFHGLKMLQNLTA 229
CC 179 DNTYITSPGLPSLTLEHLDGNKISRVDASLGLNNLAKLGLSFNSISAVDNG--SL 235
CC 230 HNTLRKMPPRVPAHQLYLDSNKKIETIPNGYFKSPFNLAIFRLANNKLT--DRGLPKNS 287
CC 236 ANTPHRLHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNTISVGSSDPCP 284

```

```

DB 288 FNISNLVTLHSHNRISVP--AINNRLEHLNHNNTISEKINGTOICP 333
DB
DB RESULT 28
DB PGSI_RABIT STANDARD; PRT; 135 AA.
DB ID PGSI_RABIT STANDARD; PRT; 135 AA.
DB AC 046377;
DB DT 28-FEB-2003 (Rel. 41, Created)
DB DT 28-FEB-2003 (Rel. 41, Last sequence update)
DB DE Bg1lycan (Bone/cartilage proteoglycan I) (Pg-S1) (Fragment).
DB GN BGN.
DB OS Oryctolagus cuniculus (Rabbit).
DB OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
DB OX NCBI_Taxid=9986;
DB RN [1]
DB RP SEQUENCE FROM N.A.
DB RC STRAIN=New Zealand white;
DB RX MEDLINE=99037997; PubMed=9822203;
DB RA Boylston R.H., Sciore P., Reno C.R., Marchuk L., Hart D.A.;
DB RT "Altered levels of extracellular matrix molecules MENA in healing
DB RL rabbit ligaments."
DB RL Matrix Biol. 17:371-378(1998).
DB CC -1- FUNCTION: May be involved in collagen fiber assembly (By
DB CC similarity).
DB CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
DB CC similarity).
DB CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
DB CC similarity).
DB CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
DB CC in articular cartilages.
DB CC -1- PTM: The two attached glycosaminoglycan chains can be either
DB CC chondroitin sulfate or dermatan sulfate (By similarity).
DB CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
DB CC (SLRP) FAMILY. CLASS I SUBFAMILY.
DB CC -1- SIMILARITY: Contains at least 6 leucine-rich (LRR) repeats.
DB CC
DB CC This SWISS-PROT entry is copyright. It is produced through a collaboration
DB CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
DB CC the European Bioinformatics Institute. There are no restrictions on its
DB CC use by non-profit institutions as long as its content is in no way
DB CC modified and this statement is not removed. Usage by and for commercial
DB CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
DB CC or send an email to license@isb-sib.ch).
DB CC
DB CC EMBL; AF020290; AAC39515.1; -
DB CC InterPro; IPR001611; LRR.
DB CC InterPro; IPR003591; LRR_TYP.
DB CC Pfam; PF00560; LRR; 4.
DB CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
DB CC Leucine-rich repeat.
DB CC FT NON_TER 1 1
DB CC FT REPEAT <1 15 LRR-T 4.
DB CC FT REPEAT 16 36 LRR-S 3.
DB CC FT REPEAT 37 60 LRR-T 5.
DB CC FT REPEAT 61 84 LRR-T 6.
DB CC FT REPEAT 85 107 LRR-S 4.
DB CC FT REPEAT 108 >135 LRR-T 7.
DB CC FT NON_TER 135 135
DB CC SEQUENCE 135 AA; EFDC6E74D42F5098 CRC64;
DB
DB Query Match 22.2%; Score 381; DB 1; Length 135;
DB Best Local Similarity 54.5%; Pred. No. 1.8e-20;
DB Matches 72; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
DB
DB 171 KLSYRIADNTITSIPQGLPSLTLEHLDGNKISRVDASLGLNNLAKLGLSFNSISAV 230
DB 4 KSNYLRISBAKLTGIPKDPETLANEHLHNNKIQAIELEDLRYSKLYLGLGHQIRMI 63
DB 231 DNGSLANPHLAEHLNHNKLTFRVPGGLAEHKYIQVYVYLNHNNTISVGSSDPCP 290

```

Db 64 ENGLSLEP.LPTLREHLNHNKLSRVPAQLPDLKLLQVYVLLSHNNITKGVNDPCEVFGVK 123

QY 291 KASYSVGLFSN 302

Db 124 RAYNGISLFSN 135

RESULT 29

LUM_COTJA STANDARD; PRT; 343 AA.

AC Q9DE67;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Luminan precursor (Keratan sulfate proteoglycan Luminan). (KSPG Luminan).

GN LUM OR LDC.

OS Coturnix coturnix japonica (Japanese quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.

OC NCBI_TaxID=93934;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Cornea;

RX MEDLINE=20556471; PubMed=11102759;

RA Cornup L.M., Dunley J.R., Hassell J.R., Conrad A.H., Conrad G.W.;

RT "Molecular cloning and relative tissue expression of decorin and Luminan in embryonic quail cornea."

RL Matrix Biol. 19:699-704(2000).

CC -1 SUBUNIT: Binds to laminin (By similarity).

CC -1 SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

CC -1 PTM: Binds keratan sulfate chains (By similarity).

CC -1 SIMILARITY: BELONGS TO THE SMALL LECTINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.

CC -1 SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AF125251; AAG48155.1; -

DR InterPro; IPR001611; LRR.

DR InterPro; IPR003372; LRR_Nterm.

DR InterPro; IPR003591; LRR_typ.

DR Pfam; PF00560; LRR; 10.

DR Pfam; PF01462; LRRNT; 1.

DR SMART; PR00019; LEUDICRPT.

DR SMART; SMO0369; LRR_TYP; 1.

DR SMART; SMO0013; LRRNT; 1.

KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.

FT SIGNAL 1 18

FT CHAIN 19 343

FT DOMAIN 40 56

FT REPEAT 62 81

FT REPEAT 82 105

FT REPEAT 106 131

FT REPEAT 132 152

FT REPEAT 153 176

FT REPEAT 177 201

FT REPEAT 202 222

FT REPEAT 223 246

FT REPEAT 247 271

FT REPEAT 272 291

FT REPEAT 292 321

FT REPEAT 322 343

FT DISULFID 300 333

BY SIMILARITY.

FT CARBOHYD 91 91

FT FT

FT CARBOHYD 130 130

FT FT

FT CARBOHYD 165 165

FT FT

FT CARBOHYD 257 257

FT FT

FT CARBOHYD 320 320

SO SEQUENCE 343 AA; 38642 MW; A95199CTFP32B7C4C CRC64;

Query Match 21.5%; Score 367.5; DB 1; Length 343;

Best Local Similarity 31.9%; Pred. No. 5.5e-19;

Matches 108; Conservative 58; Mismatches 146; Indels 27; Gaps 11;

QY 4 SGI-----GREVDDDDPEPSLGP---VCFRCQCHL---RVQCSGLGDKPKDLP 51

Db 14 SGIFCQYDGP--ADDYGYDP-FGSPSTAVCAPBCNCPYSTPAMYCDMLKLTIP-IVPS 69

QY 52 DTTLLDQNNKITEIKQDFFKLNALILVNNKI--SKVSPGAFPLVLERLYLSKN 109

Db 70 GIKYLYRANMIBSIBERTFNVTDLQWLLIDHNLNSKIKGAVFSGLKRLKLTINYN 129

QY 110 QLKELPERMPKTLQELRAHENEITKRVKVTENGINQIVIELGTNPLKSSGIENGAFQGM 169

Db 130 NLTEAVGFLPKTLDDLQLSHKIKITKVPNGALEGLVNLVTHLQNNQLKADSI-SGAFKGL 188

QY 170 KKLSTIRADTNITISFQGLPPSLTEHLDSNKISRDVADSLKGLNLAKLGLSPNSISA 229

Db 189 NSLYLYDSFQQLTKLPGLPHSLIMLYFDNNQISNPDEYFQGFKTLQYLRLSHNTLT- 247

QY 230 VDN---GSLANTPHLRHLNHNKLTVPGLAHHKYQVYVLLSHNNISVYSSGDFCPBG 286

Db 248 -DSGIPGVNFTSLVELDSFNQKSLP---TSENLENYLYQNNKINKRPLSPFCVYV 303

QY 287 HNTKASYSVGLFSNPNVQYWEIQSPRCVYVSAIQI 325

Db 304 GPLYTSKITHRLDGNNTLRADLPQEWYNCGLRVAAEISL 342

RESULT 30

LUM_HUMAN STANDARD; PRT; 338 AA.

AC P51884; O96OM7;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Luminan precursor (Keratan sulfate proteoglycan Luminan) (KSPG Luminan).

GN LUM OR LDC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cartilage, Intestine, and Placenta;

RX MEDLINE=95394964; PubMed=765616;

RA Grover J., Chen X.-N., Korenberg J.R., Roughley P.J.;

RT "The human Luminan gene. Organization, chromosomal location, and expression in articular cartilage."

RL J. Biol. Chem. 270:21942-21949(1995).

RN [2]

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Cornea;

RX MEDLINE=96047334; PubMed=7558030;

RA Chakravarti S., Stallings R.L., Sundarraj N., Cornuet P.K., Hassell J.R.,

RT "Primary structure of human Luminan (Keratan sulfate proteoglycan) and localization of the gene (LUM) to chromosome 12q21.3-q22.1;"

RL Genomics 27:481-488(1995).

RN [3]

RN SEQUENCE FROM N.A.

CC TISSUE-Prostate; PubMed=12477932;
 CC MEDLINE=22388257;
 CC Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 CC Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 CC Bosak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahy J., Helton E., Ketterman M., Madan A., Rodrigues A.,
 CC Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 CC Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
 CC Buterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 CC Scherch A., Schein J.E., Jones S.J.M., Maira W.A.,
 CC "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences."
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBMIT: Binds to laminin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Cornea and other tissues.
 CC -1- DEVELOPMENTAL STAGE: Present in the extracellular matrix of human
 CC articular cartilage at all ages, although its abundance is far
 CC greater in the adult. In the adult cartilage laminin exists
 CC predominantly in a glycoprotein form lacking keratan sulfate,
 CC whereas the juvenile form of the molecule is a proteoglycan.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS II SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U18728; AAA85268.1; -
 CC EMBL; U21128; AAA91639.1; -
 CC EMBL; BC007038; AAA07038.1; -
 CC Genew; HGNC:6724; LUM.
 CC MIM: 600616; -
 CC DR GO; GO:000578; C:extracellular matrix; TAS.
 CC DR GO; GO:0005203; F:proteoglycan; TAS.
 CC DR GO; GO:0007601; P:vision; TAS.
 CC DR InterPro; IPR001611; LRR.
 CC DR InterPro; IPR000372; LRR_Nterm.
 CC DR InterPro; IPR003591; LRR_Typ.
 CC DR Pfam; PF00560; LRR; 9.
 CC DR Pfam; PF01462; LRRNT; 1.
 CC DR PRINTS; PR00019; LEURICRPT.
 CC DR SMART; SMO0369; LRR_Typ; 1.
 CC DR SMART; SMO0013; LRRNT; 1.
 CC DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 CC Leucine-rich repeat; Signal.
 CC KW CHAIN 19 338 LUMICAN.
 CC FT DOMAIN 37 53 LRR-S 1.
 CC FT REPEAT 59 76 LRR-T 1.
 CC FT REPEAT 79 102 LRR-T 2.
 CC FT REPEAT 103 128 LRR-S 2.
 CC FT REPEAT 129 149 LRR-T 3.
 CC FT REPEAT 150 171 LRR-T 4.
 CC FT REPEAT 172 196 LRR-S 3.
 CC FT REPEAT 197 217 LRR-T 5.
 CC FT REPEAT 218 241 LRR-T 6.
 CC FT REPEAT 242 266 LRR-T 6.

FT REPEAT 267 286 LRR-S 4.
 FT REPEAT 287 316 LRR-T 7.
 FT REPEAT 317 338 LRR-T 8.
 FT DISULFID 295 328 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 127 127 (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 101 101 L -> P (IN REF. 1).
 FT CARBOHYD 101 101 L -> V (IN REF. 1).
 FT CARBOHYD 338 AA; 38429 MW; 905D2EBD370CC59D CRC64;
 FT SEQUENCE
 SO
 Query Match 21.3%; Score 365.5; DB 1; Length 338;
 Best Local Similarity 32.0%; Pred. No. 7.5e-19;
 Matches 106; Conservative 57; Mismatches 135; Indels 33; Gaps 12;
 13 DDDFEPRL---GVCPRRCQ---HRAVQCSDEGLDKVPRDLPDPTLLDLONNKITE 65
 22 DYDFPLSTYGSSPNCACBECNCPESYPSAMVCDLKLKSVW-VPPGIRYLYLRNNQIDH 80
 66 IKDGFKNLKNLHALLIVNKKI--SKVSPGAFTPVVKLERLYLSKNOLKEPEKPKTIQ 123
 81 IDEKAFENVTDQWILDNHNLLENKIGKGRVSKQKQKHHNNNTESVGLPKSL 140
 124 EIRAHENETTKRKVTENGDNOMVIELGTNPDKSSGIENAGFQGMKKLSYRIADYNT 183
 141 DQLTHNNITTKLG--SFGVLVLFPIHQHNKLKEDAV-SAFKGLKSLLEYLDLSPNQIA 197
 184 SIPOGLPSPILTEHLDGNKISRVDASLKGNNLAKLGLSPFISAVDN---GSLANTPH 240
 198 RPSGLPVSLLTLTYLDNNKISNIPDEYFRFPAALQYLIRSHNELA--DSGLPNSFNVS 255
 241 IREHLDDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVSSSDPCP---PCHNTKKASYS 297
 256 LVELDLSYNNKLNIP---TVNENLENYLLENVQLEKFPDKSKCKLIGP-----LSYK 306
 298 S---LFSNPVQYWEIQPSTPRCVYRSALQL 325
 307 KHLRLDGNRISSETSLPPDMYECLRVANVTL 337
 Db
 Search completed: February 9, 2004, 11:36:34
 Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 08:11:09 ; Search time 75 Seconds
(without alignments)
696.281 Million cell updates/sec

Title: US-10-004-176-6
Perfect score: 1713
Sequence: 1 VEAAGIGPEVDDRDPEPSL.....QPSTFRCVYRAAIQGNK 329

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: A_Geneseq.19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1709	99.8	331	AA42260	
2	1709	99.8	359	AA57079	Mature decorin PT-
3	1709	99.8	359	AA678511	Human decorin amin
4	1709	99.8	360	AA678286	Human decorin amin
5	1709	99.8	1388	AA889471	Novel central nerv
6	1709	99.8	1388	AA889471	Collagen/decorin f
7	1704	99.5	342	AA89439	Amino acid sequenc
8	1653	96.5	353	AA805160	Human recombinant
9	1628	95.0	347	AA834392	Sequence of human
					Human decorin prot

10	1567	91.5	305	14	AA42267	
11	1429	83.4	280	14	AA42266	
12	1186	69.2	234	14	AA42265	
13	985.5	57.5	359	16	AA87951	
14	979	57.2	368	22	AA85043	
15	979	57.2	368	24	AA839564	
16	979	57.2	368	24	AA839564	
17	979	57.2	368	24	AA839564	
18	978.5	57.1	369	16	AA87952	
19	976.5	57.0	332	16	AA87953	
20	966	56.4	368	22	AA678510	
21	965	56.3	368	11	AA805159	
22	948	55.3	186	14	AA42264	
23	943.5	55.1	379	21	AA801311	
24	943.5	55.1	379	21	AA801311	
25	943.5	55.1	379	23	AA895437	
26	943.5	55.1	379	23	AA895437	
27	943.5	55.1	379	24	AA895437	
28	943.5	55.1	379	24	AA895437	
29	943.5	55.1	379	24	AA895437	
30	943.5	55.1	379	24	AA895437	
31	943.5	55.1	379	24	AA895437	
32	943.5	55.1	379	24	AA895437	
33	943.5	55.1	379	24	AA895437	
34	943.5	55.1	379	24	AA895437	
35	943.5	55.1	379	24	AA895437	
36	943.5	55.1	379	24	AA895437	
37	943.5	55.1	379	24	AA895437	
38	943.5	55.1	379	24	AA895437	
39	941.5	55.0	379	22	AA440351	
40	941.5	55.0	379	22	AA440351	
41	927.5	54.1	332	22	AA822569	
42	925.5	54.0	373	23	AA805347	
43	925.5	54.0	373	23	AA805347	
44	742.5	43.3	423	22	AA805348	
45	735	42.9	146	20	AA59749	

ALIGNMENTS

RESULT 1	
AA42260	
ID	AA42260 standard; Protein; 331 AA.
XX	
AC	AA42260;
XX	
DT	25-MAR-2003 (updated)
DT	09-JAN-2003 (updated)
DT	28-APR-1994 (first entry)
XX	
DE	Mature decorin PT-65.
XX	
KW	leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
KW	fusion protein; maltose binding protein; tumour growth; inhibition;
KW	decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
XX	
OS	Bos sp.
XX	
PH	Key
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
XX	
PN	NO9320202-A1.
XX	
PD	14-OCT-1993.
XX	

Location/Qualifiers
1..45
/label= N-terminal region
/note= "contains 4 Cys residues"
46..280
/label= repeat_region
/note= "contains 10 leucine-rich repeats"
281..331
/label= C-terminal_region

PF 02-APR-1993; 93WO-US03171.
XX
XX 03-APR-1992; 92US-0865652.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
PI Ruoslahti E;
DR MPI; 1993-336910/42.
DR N-PSDB; AAQ50046.
XX
XX Active fragments of protein esp. decorin - with cell regulatory
PT factor domain, useful for inhibiting cell regulatory factor
PT activity
XX
XX Claim 10; Page 36-38; 77pp; English.
XX
XX Active fragments of decorin (full-length coding sequence AAQ50046)
CC were generated by PCR and fused to Maltose Binding Protein. The
CC resulting fusion proteins were useful for inhibiting the activity of
CC a cell regulatory factor, esp. TGF-beta, and hence for treating
CC conditions associated with over-activity of the growth factor such
CC as certain tumours.
CC (Updated on 09-JAN-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 331 AA;
Query Match 99.8%; Score 1709; DB 14; Length 331;
Best Local Similarity 100.0%; Pred. No. 3,6e-145;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGPEVDDDDPEPSLGPVCPFCQCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 61
DB 4 EASGIGPEVDDDDPEPSLGPVCPFCQCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITETKDGDFKXKXNKLHALILVNNKISKVSPGAFPLVLELYLSKXQKLEPEKMPKT 121
DB 64 KITETKDGDFKXKXNKLHALILVNNKISKVSPGAFPLVLELYLSKXQKLEPEKMPKT 123
QY 122 LOELRAHENEITKVRKVTENGKLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 124 LOELRAHENEITKVRKVTENGKLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 183
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVDNGSLANTPHL 241
DB 184 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVDNGSLANTPHL 243
QY 242 RELHLDNNKLTVPVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGSVLSFS 301
DB 244 RELHLDNNKLTVPVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGSVLSFS -303
QY 302 NPVQYWEIQPSTFRVCYVRSALQLGNYK 329
DB 304 NPVQYWEIQPSTFRVCYVRSALQLGNYK 331
RESULT 2
AAV57079
ID AAV57079 standard; protein; 359 AA.
AC
XX AAV57079;
XX
XX 28-FEB-2000 (first entry)
XX
XX Human decorin amino acid sequence.
XX
XX Neglected target tissue antigen; NRTA; autoimmunity; autoimmune response;
KM immunotherapeutic agent; insulin dependent diabetes mellitus;
KM multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
KM uveoretinitis; inflammatory response.
XX

OS Homo sapiens.
XX
XX MO9956763-A1.
PN
XX 11-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-US10250.
PF
XX
XX 07-MAY-1998; 98US-0084636.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX Kaufman DL, Tian J, Olcott A;
PI MPI; 2000-052905/04.
XX
XX
PT Administration of neglected target tissue antigens to modulate immune
PT responses -
XX
XX Disclosure; Page 26; 79pp; English.
XX
XX Amino acid sequences AAV57063-Y57091 are examples of neglected target
CC tissue antigens NRTAa. NRTAa are antigens (whole antigens or fragments)
CC not involved in autoimmunity. These peptides and proteins are used in
CC the method of the invention which involves administering an NRTA as an
CC antigen based immunotherapeutic agent, to a host afflicted with an
CC autoimmune response associated with an autoimmune disease. The
CC immunotherapeutic agent is used to treat autoimmune diseases such as
CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
CC inflammatory immune responses. The NRTA induces regulatory tolerance by
CC elicitation of regulatory T cells among T cells recognizing the NRTA but
CC not participating in the immune response. The NRTA are capable of
CC recognition by substantial populations of uncommitted T cells which can
CC be primed, or biased, towards regulatory responses to provide effective
CC treatment. The NRTA are effective in regulating undesirable immune
CC responses even when target determinants used as agents promoting
CC tolerance agents have failed to induce an effective regulatory T cell
CC response. NRTAa as agents promoting tolerance are anticipated to be safer
CC than use of target determinants.
XX
XX
SQ Sequence 359 AA;
Query Match 99.8%; Score 1709; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 4e-145;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGPEVDDDDPEPSLGPVCPFCQCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 61
DB 32 EASGIGPEVDDDDPEPSLGPVCPFCQCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 91
QY 62 KITETKDGDFKXKXNKLHALILVNNKISKVSPGAFPLVLELYLSKXQKLEPEKMPKT 121
DB 92 KITETKDGDFKXKXNKLHALILVNNKISKVSPGAFPLVLELYLSKXQKLEPEKMPKT 151
QY 122 LOELRAHENEITKVRKVTENGKLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 152 LOELRAHENEITKVRKVTENGKLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVDNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVDNGSLANTPHL 271
QY 242 RELHLDNNKLTVPVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGSVLSFS 301
DB 272 RELHLDNNKLTVPVGGIAEHKTIQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGSVLSFS 331
QY 302 NPVQYWEIQPSTFRVCYVRSALQLGNYK 329
DB 332 NPVQYWEIQPSTFRVCYVRSALQLGNYK 359
RESULT 3

ID	Accession	Protein Name	Sequence
AG78511	standard	protein; 359 AA.	
AC	AG78511		
AD	29-JAN-2002	(first entry)	
AE		Human decorin amino acid sequence.	
AF		Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;	
AG		TGF-beta; Transforming growth factor-beta; Burn, Wound; Cystostatic;	
AH		Neurotropic; Antihemetic; Antiarthritic; Vasotropic; Vulnary	
AI		Antiartherosclerotic; Hepatotropic; Cardiant; Dermatological;	
AJ		Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;	
AK		Adult respiratory distress syndrome; Cancer; Fibrotic.	
AL		Homio sapiens.	
AM		Key	Location/Qualifiers
AN		Peptide	1..30
AO		Protein	/label= Signal_peptide
AP			31..359
AQ			/label= Mature_human_decorin
AR	US6277812-B1.		
AS	21-AUG-2001.		
AT	02-JUN-1995;	95US-0458634.	
AV	14-NOV-1991;	91US-0792192.	
AW	17-NOV-1992;	92US-0978931.	
AX	08-SEP-1994;	94US-0303238.	
AY	28-JUN-1988;	88US-0212702.	
AZ	22-JAN-1990;	90US-0467888.	
BA	13-MAY-1992;	92US-0682345.	
BB	(BURN-) BURNHAM INST.		
BC	Ruoslathi EI, Yamaguchi Y;		
BD	WPI; 2001-610491/70.		
BE		Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity	
BF		in the treatment of dermal wounds and cancer	
BG		Example 8; Fig 11; 40pp; English.	
BH		The invention relates to the inhibition of transforming growth	
BI		factor-beta (TGF-beta) activity involving contacting TGF-beta with a	
BJ		purified polypeptide comprising leucine-rich amino acid sequence of a	
BK		member of decorin superfamily of mammalian proteoglycans. The following	
BL		activities can be attributed to the polypeptide of the invention:	
BM		cytostatic, nephrotropic, antineumatic, antiarthritic, vasotropic,	
BN		antiarteriosclerotic, hepatotropic, cardiant, dermatological and	
BO		vulnary. Polypeptides of the invention act as transforming growth	
BP		factor-beta (TGF-beta) binder. The polypeptides of the invention can be	
BQ		used for treating a pathology, particularly proliferative pathology	
BR		caused by a transforming growth factor-beta (TGF-beta) regulated	
BS		activity such as cancer; particularly fibrotic cancer, fibrotic	
BT		disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis,	
BU		adult respiratory distress syndrome, cirrhosis of liver, fibrosis of	
BV		lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty	
BW		restenosis, renal interstitial fibrosis and certain dermal fibrotic	
BX		conditions such as keloids and scarring resulting from burn injuries;	
BY		other invasive skin injuries and reconstructive surgery. The wounds	
BZ		treated with the polypeptide, particularly decorin exhibit no detectable	
CA		scarring, and are histologically normal. The current sequence represents	
CB		human decorin.	
CC			
CD			
CE			
CF			
CG			
CH			
CI			
CJ			
CK			
CL			
CM			
CN			
CO			
CP			
CQ			
CR			
CS			
CT			
CU			
CV			
CW			
CX			
CY			
CA			
CB			
CC			
CD			
CE			
CF			
CG			
CH			
CI			
CJ			
CK			
CL			
CM			
CN			
CO			
CP			
CQ			
CR			
CS			
CT			
CU			
CV			
CW			
CX			
CY			
CA			
CB			
CC			
CD			
CE			
CF			
CG			
CH			
CI			
CJ			
CK			
CL			
CM			

	Best Local Similarity	100.0%	Pred. No. 4e-145;		Matches 328;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	EASGIGEVPPDDRRFEPSPGLGVPVCPFCRCQCHLRVQCSDLGIDKVPKDLPPDTLLDLQNN	61										
Db	32	EASGIGEVPPDDRRFEPSPGLGVPVCPFCRCQCHLRVQCSDLGIDKVPKDLPPDTLLDLQNN	91										
Qy	62	KITEIKQDGFKNLKNLHALILVNNKISKVSPGAFPLVKLERLYLSKNQLKELPEKMPKT	121										
Db	92	KITEIKQDGFKNLKNLHALILVNNKISKVSPGAFPLVKLERLYLSKNQLKELPEKMPKT	151										
Qy	122	LOELRAHENETTKRKTKTENGFLNOMIYIEIGTNPDLKSSGIENGAFPOGKKLSYRIRADTN	181										
Db	152	LOELRAHENETTKRKTKTENGFLNOMIYIEIGTNPDLKSSGIENGAFPOGKKLSYRIRADTN	211										
Qy	182	ITTSIPQGLPSELTEHLADGNKISRVDASLKLGNLNAKLGLSFNSISAVDNGSLANTPHL	241										
Db	212	ITTSIPQGLPSELTEHLADGNKISRVDASLKLGNLNAKLGLSFNSISAVDNGSLANTPHL	271										
Qy	242	RELHLDNNKLTRVPGVGLAEHKYIOVVYLHNNNISVVGSSDFCPGPHNTKASYSGVSLFS	301										
Db	272	RELHLDNNKLTRVPGVGLAEHKYIOVVYLHNNNISVVGSSDFCPGPHNTKASYSGVSLFS	331										
Qy	302	NPQVYWEIQTSTFCVYVRSALQIGANYK 329											
Db	332	NPQVYWEIQTSTFCVYVRSALQIGANYK 359											
RESULT 4													
AAU87286													
ID	AAU87286	standard;	Protein; 360 AA.										
AC	AAU87286;												
XX													
DT	05-JUN-2002	(first entry)											
XX													
DE	Novel central nervous system protein #196.												
XX													
KM	Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;												
KM	hyperlipoproteinemia; neoplasia; cardiovascular disorder;												
KM	cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;												
KM	nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;												
KM	acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;												
KM	endocrine disorder; reproductive system disorder; testicular feminization;												
KM	respiratory disorder; renal disorder; kidney failure; neovascularization;												
KM	myocardial infarction; wound healing; cell proliferation; skin aging;												
KM	food additive; food preservative; gene therapy.												
OS	Homo sapiens.												
XX													
PN	WO200155318-A2.												
PD	02-AUG-2001.												
XX													
PF	17-JAN-2001; 2001WO-US01332.												
XX													
XX	31-JAN-2000; 2000US-0179065.												
PR	04-FEB-2000; 2000US-0180628.												
PR	24-FEB-2000; 2000US-0184664.												
PR	02-MAR-2000; 2000US-0186350.												
PR	16-MAR-2000; 2000US-0189874.												
PR	17-MAR-2000; 2000US-0190076.												
PR	18-APR-2000; 2000US-0198123.												
PR	19-MAY-2000; 2000US-0205515.												
PR	07-JUN-2000; 2000US-0209467.												

PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227187.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231415.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.

PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249254.
PR 17-NOV-2000; 2000US-0249255.
PR 17-NOV-2000; 2000US-0249257.
PR 17-NOV-2000; 2000US-0249259.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PR (HUMA-) HUMAN GENOME SCT INC.
PR Rosen CA, Barash SC, Ruben SM;
PR
PR WPI: 2001-581633/65.
PR N-PSDB, ABK43616.
PR
PR New isolated nucleic acid encoding a protein for diagnosing,
PR preventing, treating or ameliorating medical conditions and used as
PR food additives or preservatives -
PR
PR Claim 9; SEQ ID No 804; 837pp; English.
PR
PR
PR The invention describes an isolated nucleic acid molecule (I) encoding a
PR novel central nervous system protein. (I) and polypeptides (II) encoded
PR by (I), are used to treat a medical conditions and in diagnosis of a
PR pathological condition. Disorders which are diagnosed or treated include
PR autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
PR disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
PR e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
PR angiogenesis, nervous system disorders e.g. Alzheimer's disease and
PR amyotrophic lateral sclerosis, infections caused by bacteria, viruses
PR e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
PR e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
PR adenocarcinomas and irritable bowel syndrome, reproductive system

disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 99.8%; Score 1709; DB 22; Length 360;

Best Local Similarity 100.0%; Pred. No. 4e-145; Mismatches 0; Gaps 0; Matches 328; Conservative 0; Indels 0;

QY 2 EASGIGPEVDDRDPEPSLGVPVPCQCCHLRVQCSDGLDVKVPDLPDPTLLDQNN 61
DB 33 EASGIGPEVDDRDPEPSLGVPVPCQCCHLRVQCSDGLDVKVPDLPDPTLLDQNN 92
QY 62 KITEIKDGPKNLKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKT 121
DB 93 KITEIKDGPKNLKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKT 152
QY 122 LQELRAHENEITVRKVTENGQNVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 153 LQELRAHENEITVRKVTENGQNVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 212
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGINLAKLGLSNYSISAVDNGSLANTPHL 241
DB 213 ITSIPQGLPPSLTEHLHDGKISRVDASLKGINLAKLGLSNYSISAVDNGSLANTPHL 272
QY 242 RELHLNNKLTTRPGGLAEHKYIQVYVLIHNNNISVVGSSDFPCPGHNTKASYSGLSFS 301
DB 273 RELHLNNKLTTRPGGLAEHKYIQVYVLIHNNNISVVGSSDFPCPGHNTKASYSGLSFS 332
QY 302 NPQVWEIQPSTFRVCYVRSALQGNKY 329
DB 333 NPQVWEIQPSTFRVCYVRSALQGNKY 360

RESULT 5
AAR89471
ID AAR89471 standard; Protein; 1388 AA.

XX AAR89471;

XX 01-OCT-1996 (first entry)

XX Collagen/decorin fusion protein.

KW Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
KM bone formation; tissue repair; fusion protein.

XX Synthetic.

OS Key location/Qualifiers

FT Domain 1.1057 /label= Collagen-IA

FT Peptide /note= "collagen IA alpha-helical domain"

FT Domain /label= linker_peptide

FT Misc-difference 887 /label= Decorin

FT Misc-difference 890 /note= "unidentified amino acid"

XX CA2151547-A.

XX 11-DEC-1995.

PF 12-JUN-1995; 95CA-2151547.

XX 10-JUN-1994; 94US-0259263.

XX (USSU) US SURGICAL CORP.

PI Espino P, Gruskin EA;

DR WPI; 1996-140144/15.

DR N-PSDB; AAT16517.

XX Chimeric DNA encoding protein contg. extracellular matrix protein

PT domain - and cellular regulatory factor domain, partic. useful as

PT osteogenic agents, also related vectors, transformed cells and

XX chimeric proteins.

PS Disclosure, Fig 7; 59pp; English.

XX A fusion protein (AAR89471) comprises the alpha-helical region of

CC human collagen I(a) linked to human derman sulphate proteoglycan

CC (decorin). It can be expressed in Escherichia coli transformants

CC carrying a vector incorporating a chimeric gene (AAT16517) coding for

CC the fusion. The decorin binds to type I collagen and thus affects

CC Eibx11 formation. It inhibits the cell attachment-promoting

CC activity of collagen and fibrinogen by binding to such molecules

CC near their cell binding sites. The collagen moiety provides an

CC integral substratum or scaffolding for the decorin. The fusion

XX protein acts to reduce scarring of healing tissue.

XX Sequence 1388 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 99.8%; Score 1709; DB 17; Length 1388;

Best Local Similarity 100.0%; Pred. No. 2.9e-144; Mismatches 0; Gaps 0;

Matches 328; Conservative 0; Indels 0;

QY 2 EASGIGPEVDDRDPEPSLGVPVPCQCCHLRVQCSDGLDVKVPDLPDPTLLDQNN 61
DB 1061 EASGIGPEVDDRDPEPSLGVPVPCQCCHLRVQCSDGLDVKVPDLPDPTLLDQNN 1120
QY 62 KITEIKDGPKNLKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKT 121
DB 1121 KITEIKDGPKNLKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKT 1180
QY 122 LQELRAHENEITVRKVTENGQNVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 1181 LQELRAHENEITVRKVTENGQNVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 1240
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGINLAKLGLSNYSISAVDNGSLANTPHL 241
DB 1241 ITSIPQGLPPSLTEHLHDGKISRVDASLKGINLAKLGLSNYSISAVDNGSLANTPHL 1300
QY 242 RELHLNNKLTTRPGGLAEHKYIQVYVLIHNNNISVVGSSDFPCPGHNTKASYSGLSFS 301
DB 1301 RELHLNNKLTTRPGGLAEHKYIQVYVLIHNNNISVVGSSDFPCPGHNTKASYSGLSFS 1360
QY 302 NPQVWEIQPSTFRVCYVRSALQGNKY 329
DB 1361 NPQVWEIQPSTFRVCYVRSALQGNKY 1388

RESULT 6
AAV84539
ID AAV84539 standard; Protein; 1388 AA.

XX AAV84539;

XX 25-JUL-2000 (first entry)

XX Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.

KW Extracellular matrix protein; self aggregation; hydroxylated proline;

KM trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;

KW collagen; fibrinogen; fibronectin; post translational hydroxylation;

KM decorin; chimera.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.
 XX
 FH Key
 FT Misc-difference 87 Location/Qualifiers
 FT /note= "Gly encoded by GCG"
 FT Misc-difference 305 /note= "Glu encoded by CAA"
 FT /note= "Gly encoded by CAA"
 FT Misc-difference 363 /note= "Gly encoded by CGT"
 FT /note= "Gly encoded by CGT"
 FT Misc-difference 378 /note= "Glu encoded by GGT"
 FT /note= "Gly encoded by GGT"
 FT Misc-difference 429 /note= "Gly encoded by CGA"
 FT /note= "Gly encoded by CGA"
 FT Misc-difference 444 /note= "Gly encoded by GCG"
 FT /note= "Gly encoded by GCG"
 FT Misc-difference 543 /note= "Gly encoded by GCC"
 FT /note= "Gly encoded by GCC"
 FT Misc-difference 546 /note= "Gly encoded by GCT"
 FT /note= "Gly encoded by GCT"
 FT Misc-difference 606 /note= "Gly encoded by GAC"
 FT /note= "Gly encoded by GAC"
 FT Misc-difference 702 /note= "Gly encoded by CGT"
 FT /note= "Gly encoded by CGT"
 FT Misc-difference 815 /note= "Pro encoded by CTT"
 FT /note= "Pro encoded by CTT"
 FT Misc-difference 858 /note= "Gly encoded by GCT"
 FT /note= "Gly encoded by GCT"
 FT Misc-difference 1066 /note= "Gly encoded by GCC"
 FT /note= "Gly encoded by GCC"
 XX
 PN EP992586-A2.
 XX
 PD 12-APR-2000.
 XX
 PF 07-OCT-1999; 99EP-0119184.
 XX
 PR 09-OCT-1998; 98US-0169768.
 XX
 PA (USU) US SURGICAL CORP.
 XX
 PI Gruskin EA, Buechter DD, Zhang G, Connolly K;
 XX WPI, 2000-259138/23.
 DR N-PSDB; AAI12499.
 XX
 XX Production of extracellular matrix proteins containing
 PT 4-trans-hydroxyproline results in native self aggregating proteins,
 PT useful on medical implants -
 XX
 PS Claim 25; Fig 17A-B; 260pp; English.
 XX
 CC The specification describes a method for producing an extracellular
 CC matrix protein or its fragment. The extracellular matrix protein is
 CC capable of self aggregating in a cell which does not ordinarily
 CC hydroxylated prolines. The method comprises optimising a nucleic acid
 CC sequence for expression in the cell by substitution of codons preferred
 CC by that cell for naturally occurring codons not preferred by the cell;
 CC incorporating the nucleic acid sequence into the cell; and contacting
 CC the cell with a hypertonic growth medium containing at least one amino
 CC acid, selected from the group consisting of trans-4-hydroxyproline and
 CC 3-hydroxyproline to allow at least one of the amino acids to be
 CC assimilated into the cell and incorporated into the extracellular matrix
 CC protein. The method may be used to make host cells assimilate and
 CC incorporate trans-4-hydroxyproline into proteins. This is especially
 CC useful in the recombinant production of proteins such as collagen,
 CC fibrinogen and fibronectin whose ability to self aggregate and produce
 CC functional proteins depends on the post translational hydroxylation of
 CC proline. The method is also useful in studying the structure and function
 CC of polypeptides which do not normally contain trans-4-hydroxyproline.
 CC The present sequence represents a chimeric collagen 1 (alpha1)/decorin

CC protein, which may be produced using the method of the invention.
 XX
 SQ Sequence 1388 AA;
 XX
 Query Match 99.8%; Score 1709; DB 21; Length 1388;
 Best Local Similarity 100.0%; Pred. No. 2,9e-144;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EASGIGPEVDDRDPEFSLGVCPEFRQCHLRVQCSDLGLDKVKKLPPTTLTLDLQNN 61
 DB 1061 EASGIGPEVDDRDPEFSLGVCPEFRQCHLRVQCSDLGLDKVKKLPPTTLTLDLQNN 1120
 QY 62 KITEIKKGDPRKKNLKNHALLVNNKISKVSPGAFPTLVKLERLYLSNQLKEPKPKPT 121
 DB 1121 KITEIKKGDPRKKNLKNHALLVNNKISKVSPGAFPTLVKLERLYLSNQLKEPKPKPT 1180
 QY 122 LQELRAHENETTKVRKVTFNGLNQMYIEIGTPTLKSSGIENGAFOGKKLSYRIADTN 181
 DB 1181 LQELRAHENETTKVRKVTFNGLNQMYIEIGTPTLKSSGIENGAFOGKKLSYRIADTN 1240
 QY 182 ITSIPQGLPSSLTEHLMDGNKISRVDASLKGNNLAKLGLSFNSISAVNGSLANTPHL 241
 DB 1241 ITSIPQGLPSSLTEHLMDGNKISRVDASLKGNNLAKLGLSFNSISAVNGSLANTPHL 1300
 QY 242 RELHLDNNKLTVPDGLAEHKYIQVYVLNNNNISVSSSPCPGHTTKASVSGVLSFS 301
 DB 1301 RELHLDNNKLTVPDGLAEHKYIQVYVLNNNNISVSSSPCPGHTTKASVSGVLSFS 1360
 QY 302 NPVOYWEIOPSTFRCVYVRSALQLGNKY 329
 DB 1361 NPVOYWEIOPSTFRCVYVRSALQLGNKY 1388
 XX
 RESULT 7
 AAR89439
 ID AAR89439 standard; Protein; 342 AA.
 XX
 AC AAR89439;
 XX
 DT 20-AUG-1996 (first entry)
 XX
 DE Human recombinant decorin.
 XX
 KM Decorin; PG-II; PG-40; proteoglycan; guanidinium ion.
 XX
 OS Homo sapiens.
 OS
 FH Key
 FT Peptide 1..14 Location/Qualifiers
 FT /label= Sig_peptide
 XX
 PN WO9601842-A1.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08542.
 XX
 PR 08-JUL-1994; 94US-0272919.
 XX
 PA (JUL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Craig WS, Harper JR, Hernandez SD, Kostel PJ, Parker JR,
 PI Vedvick JS;
 XX WPI, 1996-097586/10.
 DR N-PSDB; AAT10741.
 XX
 PT Purificn. of human recombinant decorin - using a strong anion
 PT exchange resin, a hydrophobic interaction chromatography resin and a
 PT strong anion exchange resin
 XX
 PS Disclosure; Fig 1A-D; 55pp; English.
 XX

CC Human recombinant decorin (AAR89439) was obtd. by expression of a
CC cDNA clone (AAR10741) in CHO host cells. Decorin (or PGII or PG-40)
CC is a proteoglycan having a 40 kDa core protein. Recombinant
CC decorin can be produced by cotransfection of CHO-DG4 cells with
CC pSV2-decorin and pSV2ohfr. Large-scale cultures can be performed
CC using CHO cells attached to microcarrier beads. The recombinant
CC protein is purified from the cells using a 3-step chromatographic
CC procedure. It can be used for the highly sensitive detection of
CC guanidinium ions (ppm range), partic. in protein-contg. solns.
CC purified using GdnCl, and also has therapeutic applns.

XX Sequence 342 AA;

Query Match 99.5%; Score 1704; DB 17; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 16 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 75

QY 62 KITETIDGPFKLNKLNHALILVNNKISKVSPGAFPLVLYLERLYLSKNQKELPEKMPKT 121
DB 76 KITETIDGPFKLNKLNHALILVNNKISKVSPGAFPLVLYLERLYLSKNQKELPEKMPKT 135

QY 122 LQELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGMKKLSYIRIADTN 181
DB 136 LQELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGMKKLSYIRIADTN 195

QY 182 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 255

QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFCPGHNTKKAASYSGVSLFS 301
DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFCPGHNTKKAASYSGVSLFS 315

QY 302 NPVOYWEIOPSTFRCYVRSATQLGNYK 328
DB 316 NPVOYWEIOPSTFRCYVRSATQLGNYK 342

RESULT 8

AAR05160 standard; protein; 353 AA.

AC AAR05160;

DT 25-MAR-2003 (updated)

DT 17-DEC-2001 (updated)

DT 09-OCT-1990 (first entry)

DE Sequence of human bone proteoglycan II (decorin).

XX Osteoporosis; rheumatoid arthritis; Paget's disease;

KM atherosclerosis; periodontal; human bone matrix; proteoglycan.

XX Homo sapiens.

XX USN7432044-N.

XX 17-APR-1990.

XX 03-NOV-1989; 89US-0142159.

XX 03-NOV-1989; 89US-0142159.

XX (USSH) NAT INST OF HEALTH.

XX Termine J;

XX WPI; 1990-178641/23.

XX N-PSDB; AAQ04491.

XX Human bone matrix DNA and proteins -
PT used in detection, diagnosis and treatment involving skeletal
PT and/or connective tissue disease states.

XX Disclosure; Page ?; ?pp; English.

XX Probes and Abs raised to the proteins can be used to determine

CC their levels useful in diagnosis of associated connective tissue

CC diseases states such as osteoporosis, osteo/rheumatoid arthritis,

CC Paget's disease, atherosclerosis and periodontal disease.

CC Proteins may also be used to induce or block biological function.

CC (Note: Revised entry submitted to correct the patent number format of

CC US Government-owned NTIS applications to prevent clashes with ongoing US

CC granted patent numbers. For further information please visit the Derwent

CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 353 AA;

Query Match 96.5%; Score 1653; DB 11; Length 353;
Best Local Similarity 97.3%; Pred. No. 4.3e-140;

Matches 319; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 26 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 85

QY 62 KITETIDGPFKLNKLNHALILVNNKISKVSPGAFPLVLYLERLYLSKNQKELPEKMPKT 121
DB 86 KITETIDGPFKLNKLNHALILVNNKISKVSPGAFPLVLYLERLYLSKNQKELPEKMPKT 145

QY 122 LQELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGMKKLSYIRIADTN 181
DB 146 LQELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGMKKLSYIRIADTN 205

QY 182 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 241
DB 206 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 265

QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFCPGHNTKKAASYSGVSLFS 301
DB 266 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFCPGHNTKKAASYSGVSLFS 325

QY 302 NPVOYWEIOPSTFRCYVRSATQLGNYK 329
DB 326 NPVOYWEIOPSTFRCYVRSATQLGNYK 353

RESULT 9

AAE34392 standard; Protein; 347 AA.

AC AAE34392;

DT 14-MAY-2003 (first entry)

DE Human decorin protein.

XX Human; diagnosis; osteoarthritis; rheumatoid arthritis; decorin.

XX Homo sapiens.

XX WO200295415-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-EP05612.

(OSTE-) OSTEOMETER BIO TECH AS.

XX Christgau S, Henriksen DB, Cloos PAC;
XX WPI; 2003-140389/13.
XX An assay for the diagnosis or assessment of the severity of
XX osteoarthritis or rheumatoid arthritis comprising detecting an
XX isomerized or optically inverted protein in a sample -
XX
XX Disclosure; Page 68-70; 106pp; English.
XX
XX The invention relates to an assay for the diagnosis or assessment of
XX the severity of osteoarthritis or rheumatoid arthritis. The assay
XX involves measuring (in a biological sample) the amount or presence of
XX an isomerized or optically inverted protein or one or more isomerized
XX or optically inverted fragments from proteins such as perlecan,
XX biglycan, decorin, fibrillin-1 or procadherin. The assay is useful
XX for the diagnosis or assessment of the severity of osteoarthritis or
XX rheumatoid arthritis. The present sequence is human decorin protein.
XX
XX Sequence 347 AA;
SQ
Query Match 95.0%; Score 1628; DB 24; Length 347;
Best Local Similarity 96.3%; Pred. No. 7,4e-138;
Matches 316; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
XX
QY 2 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB |||||
32 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 91
QY KITEIKGDFKRNKLNHALILVNNKISKVSPGAFPLVLERLYLSKNQKLEPERKPKT 121
DB |||||
92 KITEIKGDFKRNKLNHALILVNNKISKVSPGAFPLVLERLYLSKNQKLEPERKPKT 151
QY 122 LOELRAHENEITKRVKTYFNGLNQMIYIELGTNPPLKSSGIENGAFOGKKLSYIRIADTN 181
DB |||||
152 LOELRAHENEITKRVKTYFNGLNQMIYIELGTNPPLKSSGIENGAFOGKKLSYIRIADTN 211
QY 182 ITSIPQGLPSSLTELHLDGNNKISRVDAAASLKGANNLAKGLSFNSISAVDNGSLANTPHL 241
DB |||||
212 ITSIPQGLPSSLTELHLDGNNKISRVDAAASLKGANNLAKGLSFNSISAVDNGSLANTPHL 271
QY 242 RELHLDNNKLTTRVPGGLAHEKTYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 301
DB |||||
272 RELHLDNNKLTTRVPGGLAHEKTYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 319
QY 302 NPVOYWEIOPSTFRVCYVRSALIQGNKY 329
DB |||||
320 NPVOYWEIOPSTFRVCYVRSALIQGNKY 347

RESULT 10
AAR42267
ID AAR42267 standard; Protein; 305 AA.
XX
AC AAR42267;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 28-APR-1994 (first entry)
XX
DE Decorin sequence PT-78 (N-terminal to half C-terminal).
XX
XX leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
XX fusion protein; maltose binding protein; tumour growth; inhibition;
XX decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
OS Bos sp.
XX
XX WO9320202-A1.
XX
XX 14-OCT-1993.
XX

PF 02-APR-1993; 93WO-US03171.
XX
XX 03-APR-1992; 92US-0865652.
XX
XX (JOL-) LA JOLLA CANCER RES FOUND.
XX
XX Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
XX Rostaletti E;
XX
XX WPI; 1993-336910/42.
XX
XX N-PSDB; AAQ50053.
DR
XX
XX Active fragments of protein esp. decorin - with cell regulatory
XX factor domain, useful for inhibiting cell regulatory factor
XX activity
XX
XX Claim 10; Page 49-50; 77pp; English.
XX
XX Active fragments of decorin (full-length coding sequence AAQ50046)
XX were generated by PCR and fused to Maltose Binding Protein. The
XX resulting fusion proteins were useful for inhibiting the activity of
XX a cell regulatory factor, esp. TGF-beta, and hence for treating
XX conditions associated with over-activity of the growth factor such
XX as certain tumours
XX
XX (Updated on 09-JAN-2003 to add missing OS field.)
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
SQ
Sequence 305 AA;
Query Match 91.5%; Score 1567; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-132;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB |||||
4 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITEIKGDFKRNKLNHALILVNNKISKVSPGAFPLVLERLYLSKNQKLEPERKPKT 121
DB |||||
64 KITEIKGDFKRNKLNHALILVNNKISKVSPGAFPLVLERLYLSKNQKLEPERKPKT 123
QY 122 LOELRAHENEITKRVKTYFNGLNQMIYIELGTNPPLKSSGIENGAFOGKKLSYIRIADTN 181
DB |||||
124 LOELRAHENEITKRVKTYFNGLNQMIYIELGTNPPLKSSGIENGAFOGKKLSYIRIADTN 183
QY 182 ITSIPQGLPSSLTELHLDGNNKISRVDAAASLKGANNLAKGLSFNSISAVDNGSLANTPHL 241
DB |||||
184 ITSIPQGLPSSLTELHLDGNNKISRVDAAASLKGANNLAKGLSFNSISAVDNGSLANTPHL 243
QY 242 RELHLDNNKLTTRVPGGLAHEKTYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 301
DB |||||
244 RELHLDNNKLTTRVPGGLAHEKTYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 303
QY 302 NP 303
DB |||||
304 NP 305

RESULT 11
AAR42266
ID AAR42266 standard; Protein; 280 AA.
XX
AC AAR42266;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 28-APR-1994 (first entry)
XX
DE Decorin sequence PT-77 (N-terminal to LR10).
XX
XX leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
XX fusion protein; maltose binding protein; tumour growth; inhibition;
XX decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
XX

XX	Rattus sp.
OS	
XX	
FH	Key Location/Qualifiers 1..37
FT	Peptide /label= Sig_peptide
FT	Region 44..60
FT	/label= Hypervariable_region
XX	
PX	
MN	MO95J0432-AL.
PD	
XX	16-NOV-1995.
PE	
PR	09-MAY-1994; 94WO-EP01479.
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
PI	Hagenochrl R, Huston J, Junghans U, Kappler J, Koops A; Mueller HW;
DR	WI; 1995-403938/51.
N-	N-PSDB; AAT08768.
PT	Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) - for mainthin structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
XX	
PS	Claim 1; Page 44-45; 60pp; English.
CC	Rat biglycan (AA87951) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. Recombinant biglycan, obcd. by expression of encoding cDNA (AAT08768) in eukaryotic host cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with dementia.
SQ	Sequence 369 AA:
Query Match	57.5%; Score 985.5; DB 16; Length 369;
Best Local Similarity	57.6%; Pred. No. 5, 2e-80;
Matches 190; Conservative	51; Mismatches 86; Indels 3; Gaps 2
Dy	2 EASGIGPP--YDDDDDFEPSLGPVPFPFCQCGLLRVVOCSDLGDVKYPKDPDPTTLIDLQ 59
Dd	40 EASSGGDTTSGVDLDLSLTPTSAMCPFGCHCLRVVOCSDDLCKTVPKRISIDPTLLDIQ 99
Oy	NNKTIEIKDGPFKNLNKLHALIVNNKISKVSPGAFTPVLVKLERLYLINSOLKELPKMXP 119
Dd	100 NNNDIELAKDKPGKGLOHLVALYLVNANKSKIRKXAFFSPRLKOQLYSISGNILVELIPNPINP 159
Oy	120 KTLQELRAHENETITVRKYTFNGNLNQMTIVIELGTNPPLXSSSIENGAFQGMKKLSYIRIAD 179
Dd	160 SSLVELRITHRRIRRKVPKFVFSGFLNMNCIEWGNPLENSGEPEGAPGL-KLVNTLRITSB 218
Oy	180 TINTSIFPGSLFRELHDGKRISRVAASLGKIANTLAAGLSTNISISAUNDGLANTP 239
Dd	219 AKLTGIKPDLPEPTLMLEHLDHKKAIAIEDLIARFSKYRIGLIGNOIRMINGELSIFLP 278
Oy	240 HURELHLNNNKLTRPVGGLAEHYIOVVYLANNNISVYGSSDFPCPHNTTKAASYGSVTL 299
Dd	279 TLREHLHNKKLSRPAGIPDLKLGVYYLHSNNNIITKVGINDFCEMGVGKRAYYNIGISTL 338
Oy	300 FSNPYQWEIFQPSTERCYVRSAILGYNYK 329
Dd	339 FNNPVPYWEOPATRCVTDRILAIGFNMYK 368

[illegible]

QY	121	TLGLRAHNEKITVRKVTPEGLNQMTVIELGTNP	KLSSGIENCAFOGMKKLSTYRIADT	180
Db	160	SLVELRLHDNRKIRKVPKGVFSGLNNMCIEG	GNPLNSGFEPAFDGL-KLNTLRISGA	218
QY	181	NITSIPQGLPEPSTLHLDGNKISRVDAA	SLKGLNNLAKGLSPNSISAVDNGSLANTPH	240
Db	219	KLGTIPDLPETLWELHLDHDKICQALEHED	LLRRSKLYRLGLGNQIRMIENGSLFLPT	278
QY	241	LREIHLDDNKKLTRVPGGLAEHKYIQVYV	LLANNNISVVGSSDPFCPPGANTKKA	300
Db	279	LREIHLDDNKKLARVPDGLPDLKQLQVY	VLHNNITKYGVDNFCPMGFVGKRAYNGISL	338
QY	301	SNPQYWEIOPSTERCYVVRSAIQGNK	329	
Db	339	NNPVPWEVOPATFRCTVDRLAIQGNK	367	
RESULT 15				
ABR39564	1D	ABR39564	standard; protein; 368 AA.	
XX	AC	ABR39564;		
XX	DE	12-JUN-2003	(first entry)	
XX	DE	Human biglycan protein sequence.		
XX	KW	DAG-125; collagen VI; DAPC; biglycan;	therapeutic; neuroprotective;	
XX	KW	human.		
XX	OS	Homo sapiens.		
XX	FH	Key	Location/Qualifiers	
FT	FT	Region	1..37	
FT	FT	Misc-difference	/note= "prepro-region"	
FT	FT	Region	/note= "encoded by CAG"	
FT	FT	Region	/note= "N-terminal cysteine-rich region"	
FT	FT	Region	81..314	
FT	FT	Region	/note= "TLR region"	
FT	FT	Region	315..368	
FT	FT		/note= "C-terminal cysteine-rich region"	
XX	PN	WO2003015615-A2.		
XX	PD	27-FEB-2003.		
XX	PF	15-AUG-2002; 2002MO-US26201.		
XX	PR	15-AUG-2001; 2001US-312551P.		
XX	PA	(UYBR-) UNIV BROWN RES FOUND.		
XX	PI	Fallon JR, Rafii M;		
XX	DR	WPI; 2003-278504/27.		
XX	DR	N-PSDB; ABZ76353, ABZ76354.		
XX	PT	Stabilizing collagen VI-dependent	dystrophin-associated protein	
XX	PT	complexes on the surface of a cell	for preparing a composition for	
XX	PT	treating neuromuscular or	neurological disease by contacting the cell	
XX	PS	with biglycan therapeutic		
XX	PS	Claim 8; Page 122-123; 123pp;	English.	
XX	CC	The invention relates to stabilizing	collagen VI-dependent dystrophin-	
XX	CC	associated protein complexes (DAPCs)	on the surface of a cell. The	
XX	CC	method involves contacting the cell	with biglycan therapeutic. The	
XX	CC	method is useful for preparing a	composition for treating neuromuscular	
XX	CC	or neurological disease. The present	sequence represents a human biglycan	
XX	CC	protein sequence.		

SO	Sequence	368 AA;
Query Match	57.2%; Score 979; DB 24; Length 368;	
Best Local Similarity	57.4%; Pred. No. 2e-79;	
Matches	189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;	
DG	2 EASGIPE-VPDDDFEPLSGVPCFFCQCHLRVQSCSDGLDLPKDLPPDTLLDLO 60	
OY	40 EASADNSGVLDPSVSPTTYSAMCPFGCHHTRVQSSDGLSKVPEISPTDLLDLO 99	
DG	61 NKITEIKDGEPKNLKHALLVNKKISKVSPGFATVLKERLYLSRNOLKEIPKMPK 120	
OY	100 NDISELRNDPKGHLYALVALVNKKISKIEKAFSPLRLQKLQYISKIHLVEIPNIPS 159	
DG	121 TLQELRAHEKITRVKRYTFNGLNOMIVIELGTMLKSSGGIENAGFQGMKLSTIRIADT 180	
OY	160 SLVERIRHDNRIRKVPKGVFGLNMNCIEMGNPNLENSGEPAFDGL-KLVTLRISEA 218	
DG	219 KLTIPIPOLPSSLTELHLDGDKISRVAASLKGNNTIAKGLSFENSISAVDNGSLANTPH 240	
OY	241 LRELHLDNNKLTTRVPGILAERKYIQVYYLHNNTISVYGSDFCEPGHNTKKAISGVSLF 300	
DG	279 LRELHLDNNKLTARVPSGLPDKLQVYYLHSNNTITKVGVNFCEPMGFVKAAVYGISLF 338	
OY	301 SNPOVWEIQPSTRFCVTVRSAILQLGNTK 329	
DG	339 NNFPVYMEVQPATERCTVDRILAIQFGNK 367.	
RESULT 16		
ABR47399		
ID	ABR47399 standard; Protein; 368 AA.	
AC	ABR47399;	
XX	12-JUN-2003 (first entry)	
DE	Breast cancer associated protein sequence SEQ ID NO:29.	
KW	Human; breast cancer; cytostatic; gene therapy.	
OS	Homo sapiens.	
PX	WO2003004989-A2.	
PR	16-JAN-2003.	
PF	21-JUN-2002; 2002WO-US19669.	
PR	21-JUN-2001; 2001US-299887P.	
PR	18-JUL-2001; 2001US-305601P.	
PR	25-SEP-2001; 2001US-325002P.	
PR	05-MAR-2002; 2002US-362585P.	
PR	14-MAY-2002; 2002US-380391P.	
PA	(MILL-) MILLENIUM PHARM INC.	
PI	Lillie J, Ganavarrapu M, Glatt K, Hoersh S, Kamathar S, Mertens M,	
PI	Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE, Baat RC;	
PI	Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;	
DR	WPI; 2003-210381/20.	
DR	N-PDB; ACC50090.	
PT	Breast cancer diagnosis or treatment by comparing the level of	
PT	expression of a marker in a patient sample with that in the control	
PT	non-breast cancer sample -	
PS	Claim 1, SEQ ID 29; 126bp; English.	
XX		

CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR7366 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences
CC from the present invention have cytosolic activities and can be used in
CC gene therapy. The method is useful for diagnosing and treating breast
CC cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 368 AA;

Query Match 57.2%; Score 979; DB 24; Length 368;

Best Local Similarity 57.4%; Pred. No. 2e-79; Mismatches 88; Indels 2; Gaps 2;

Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRPFPSLGFVCPFCQCHLRVQCSDDLGLDKVPKDLPPDTLLDLON 60
DB 40 BASGADTSGVLDPPDSVTPTYSAMCFGCHLRVQCSDDLGLKSVKESIPDTLLDLON 99
QY 61 NKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTPLVKLERLYLSKNOLKELPERKMPK 120
DB 100 NDISELRKDDFKGLOHLVALVNNKISKIHEKAFSPARKIOKLYISGNHLVEIPNLS 159
QY 121 TLOELRAHENETTKYRKATFNGLNOMIYELGTNPILKSSGIEGNGAFQGMKKLSYRIADT 180
DB 160 SLVELRIHDNRIRKPKGVFSGLRMNCIEMGNGPLENSGEPGAFDGL-KLNYLRISBA 218
QY 181 NITSIPQGLPSLTELHLDGKISKVDAASLKGILNLAAGLSFNSISAVDNGSLANTPH 240
DB 219 KLITGPKDLPETLNEHLHDHKKIQAIIEEDLIRYSKLYRLGIGHNQIRMIENGSLFPT 278
QY 241 LRELHDNNKILTRVPGGLAEHKYIQVYLVHNNNISVSSSDPCPGHNTKASYSGVSLF 300
DB 279 LRELHDNNKLARVPSGLPDLKLLQVYLVHNNITKGVNDFCPMGFGVKAYNGISLIF 338
QY 301 SNPVQYWEIOPSTRCVYVRSALIQGNKY 329
DB 339 NNVPVYWEVQPATFRCTVDRALAIQGNKY 367

RESULT 17

AAE34394

ID AAE34394 standard; Protein; 368 AA.

XX AAE34394;

XX 14-MAY-2003 (first entry)

XX Human biglycan protein.

XX human; diagnosis; osteoarthritis; rheumatoid arthritis; biglycan.

XX Homo sapiens.

XX WO200295415-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-EP05612.

XX 23-MAY-2001; 2001GB-0012626.

XX (OSTE-) OSTEOMETER BIO TECH AS.

XX Christgau S, Henriksen DB, Cloos PAC;

XX WPI; 2003-140389/13.

XX An assay for the diagnosis or assessment of the severity of an
PT osteoarthritis or rheumatoid arthritis comprising detecting an
PT isomerized or optically inverted protein in a sample -
PS Disclosure; Page 71-72; 106pp; English.

CC The invention relates to an assay for the diagnosis or assessment of
CC the severity of osteoarthritis or rheumatoid arthritis. The assay
CC involves measuring (in a biological sample) the amount or presence of
CC an isomerized or optically inverted protein or one or more isomerized
CC or optically inverted fragments from proteins such as perlecan,
CC biglycan, decorin, fibrillin-1 or procadherin. The assay is useful
CC for the diagnosis or assessment of the severity of osteoarthritis or
CC rheumatoid arthritis. The present sequence is human biglycan protein.

XX Sequence 368 AA;

Query Match 57.2%; Score 979; DB 24; Length 368;

Best Local Similarity 57.4%; Pred. No. 2e-79; Mismatches 88; Indels 2; Gaps 2;

Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRPFPSLGFVCPFCQCHLRVQCSDDLGLDKVPKDLPPDTLLDLON 60
DB 40 BASGADTSGVLDPPDSVTPTYSAMCFGCHLRVQCSDDLGLKSVKESIPDTLLDLON 99
QY 61 NKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTPLVKLERLYLSKNOLKELPERKMPK 120
DB 100 NDISELRKDDFKGLOHLVALVNNKISKIHEKAFSPARKIOKLYISGNHLVEIPNLS 159
QY 121 TLOELRAHENETTKYRKATFNGLNOMIYELGTNPILKSSGIEGNGAFQGMKKLSYRIADT 180
DB 160 SLVELRIHDNRIRKPKGVFSGLRMNCIEMGNGPLENSGEPGAFDGL-KLNYLRISBA 218
QY 181 NITSIPQGLPSLTELHLDGKISKVDAASLKGILNLAAGLSFNSISAVDNGSLANTPH 240
DB 219 KLITGPKDLPETLNEHLHDHKKIQAIIEEDLIRYSKLYRLGIGHNQIRMIENGSLFPT 278
QY 241 LRELHDNNKILTRVPGGLAEHKYIQVYLVHNNNISVSSSDPCPGHNTKASYSGVSLF 300
DB 279 LRELHDNNKLARVPSGLPDLKLLQVYLVHNNITKGVNDFCPMGFGVKAYNGISLIF 338
QY 301 SNPVQYWEIOPSTRCVYVRSALIQGNKY 329
DB 339 NNVPVYWEVQPATFRCTVDRALAIQGNKY 367

RESULT 18

AAE87952

ID AAE87952 standard; Protein; 369 AA.

XX AAE87952;

XX 20-MAR-1996 (first entry)

XX Human neurotrophic biglycan.

XX Biglycan; proteoglycan; chondroitin sulphate; neuron protection;

XX neurotrophic; central nervous system; CNS; memory loss; dementia;

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..37

XX Region 44..60

XX W09530432-A1.

XX 16-NOV-1995.

PF 09-MAY-1994; 94WO-EP01479.
 XX
 PR 09-MAY-1994; 94WO-EP01479.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Hasenöhl R, Huston J, Junghans U, Kappler J, Koops A;
 PI Mueller HW;
 DR WPI; 1995-403938/51.
 XX
 PT Proteoglycan cpts., partic. chondroitin sulphate proteoglycan(s)
 PT for maintain structural and function of the CNS and attenuating
 PT memory deficit(s) in the elderly and patients with dementia
 PS Claim 3; Fig 8; 60pp; English.
 XX
 CC Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan with
 CC neurotrophic activity for brain neurons. It can be used to enhance
 CC the survival and maintain the structure and function of CNS neurons
 CC during normal ageing as well as after pathological and/or traumatic
 CC nervous system damage. It can also be used to restore function
 CC following nervous system lesions and degenerative diseases, and to
 CC improve learning efficiency and memory in the elderly and in patients
 CC with dementia.
 CC
 SQ Sequence 369 AA;
 Query Match 57.1%; Score 978.5; DB 16; Length 369;
 Best Local Similarity 57.3%; Pred. No. 2.2e-79;
 Matches 189; Conservative 51; Mismatches 87; Indels 3; Gaps 2;
 QY 2 EASGIGEE--VPDRDEPESLGPVCPFCOCHLRVVOCSDLGLKAVKDPPTTLTLDLQ 59
 DB 40 EASGADTTSGVLDPDSVTPYTSAMCPFGCHLHVVOCSDLGLKAVKDISPDTTLTLDLQ 99
 QY 60 NNKTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLEBLYSKNQLKEPEKMP 119
 DB 100 NNDISELKDDPKGLQHLVAVLVNNKISKIHEKAFSLKQLKLYISKHLEIPEPLP 159
 QY 120 KTIQELRAHENEITKVKRTFNGLNQMIIVIELGTPNPKSSGIENGAFQGMKLSYIRIAD 179
 DB 160 SSVLELRHDKRIKVPKGVSGLRNNNCEIMGNGPLENSGFEPGAFDGL-KLNYLRRISE 218
 QY 180 TNTISIPQGLPSSLTEHLDNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTP 239
 DB 219 AKLTGIPKDLPELTNELHLDHNKIOAIELEDLRYSKLYRGLGHNQIRMIENSGLSFLP 278
 QY 240 HLEHLHDNNKLTVPFGLAHKKYIOVYLLNNNISVVGSSDFCPGHNTKKASYSGVSL 299
 DB 279 TLREHLHDNNKLSRVPAGLPDLKLLQVYLLHNNITKVGVDPCMGFGVRRAYNGISL 338
 QY 300 FSNPVOYWEIOPSTFRCVYVSATQLGNKY 329
 DB 339 FNNPVPYWEVQPATFRCTDRALAIQFGNYK 368
 RESULT 19
 ID AAR87953 standard; Protein; 332 AA.
 AC AAR87953;
 DT 20-MAR-1996 (first entry)
 DE Bovine neurotrophic biglycan.
 XX
 KW Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
 KW neurotrophic; central nervous system; CNS; memory loss; dementia;
 XX learning.
 OS Bos taurus.
 XX

FH Key Location/Qualifiers
 FT Region 7..23
 XX /label= Hypervariable_region
 XX
 PN WO9530432-A1.
 XX
 PD 16-NOV-1995.
 XX
 PF 09-MAY-1994; 94WO-EP01479.
 XX
 PR 09-MAY-1994; 94WO-EP01479.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Hasenöhl R, Huston J, Junghans U, Kappler J, Koops A;
 PI Mueller HW;
 DR WPI; 1995-403938/51.
 XX
 CC Proteoglycan cpts., partic. chondroitin sulphate proteoglycan(s)
 CC for maintain structural and function of the CNS and attenuating
 CC memory deficit(s) in the elderly and patients with dementia
 PS Claim 3; Fig 8; 60pp; English.
 XX
 CC Bovine biglycan (AAR87953) is a chondroitin sulphate proteoglycan with
 CC neurotrophic activity for brain neurons. It can be used to enhance
 CC the survival and maintain the structure and function of CNS neurons
 CC during normal ageing as well as after pathological and/or traumatic
 CC nervous system damage. It can also be used to restore function
 CC following nervous system lesions and degenerative diseases, and to
 CC improve learning efficiency and memory in the elderly and in patients
 CC with dementia.
 CC
 SQ Sequence 332 AA;
 Query Match 57.0%; Score 976.5; DB 16; Length 332;
 Best Local Similarity 57.1%; Pred. No. 2.9e-79;
 Matches 188; Conservative 51; Mismatches 87; Indels 3; Gaps 2;
 QY 2 EASGIGEE--VPDRDEPESLGPVCPFCOCHLRVVOCSDLGLKAVKDPPTTLTLDLQ 59
 DB 3 EASGAEITSGIPDLDSLPYTSAMCPFGCHLHVVOCSDLGLKAVKDISPDTTLTLDLQ 62
 QY 60 NNKTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLEBLYSKNQLKEPEKMP 119
 DB 63 NNDISELRKDDPKGLQHLVAVLVNNKISKIHEKAFSLKQLKLYISKHLEIPEPLP 122
 QY 120 KTIQELRAHENEITKVKRTFNGLNQMIIVIELGTPNPKSSGIENGAFQGMKLSYIRIAD 179
 DB 123 SSVLELRHDKRIKVPKGVSGLRNNNCEIMGNGPLENSGFEPGAFDGL-KLNYLRRISE 181
 QY 180 TNTISIPQGLPSSLTEHLDNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTP 239
 DB 182 AKLTGIPKDLPELTNELHLDHNKIOAIELEDLRYSKLYRGLGHNQIRMIENSGLSFLP 241
 QY 240 HLEHLHDNNKLTVPFGLAHKKYIOVYLLNNNISVVGSSDFCPGHNTKKASYSGVSL 299
 DB 242 TLREHLHDNNKLSRVPAGLPDLKLLQVYLLHNNITKVGVDPCMGFGVRRAYNGISL 301
 QY 300 FSNPVOYWEIOPSTFRCVYVSATQLGNKY 328
 DB 302 FNNPVPYWEVQPATFRCTDRALAIQFGNY 330
 RESULT 20
 ID AAG78510 standard; protein; 368 AA.
 AC AAG78510;
 DT 29-JAN-2002 (first entry)
 XX

DE Human biglycan amino acid sequence.

XX Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;
 XX TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;
 XX Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnery
 XX Antiartherosclerotic; Hepatotropic; Cardiant; Dermatological;
 XX Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;
 XX Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.

OS Homo sapiens.

XX US6277812-B1.

XX 21-AUG-2001.

XX 02-JUN-1995; 95US-0458834.

XX 14-NOV-1991; 91US-0792192.
 XX 17-NOV-1992; 92US-0978931.
 XX 08-SEP-1994; 94US-0303238.
 XX 28-JUN-1988; 88US-0212702.
 XX 22-JAN-1990; 90US-0467888.
 XX 13-MAY-1992; 92US-0882345.

XX (BURN-) BURHAM INST.

XX Ruoslahti EI, Yamaguchi Y;
 XX WPI; 2001-610491/70.

XX Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity
 XX in the treatment of dermal wounds and cancer -
 XX Example 7; Fig 11; 40pp; English.

XX The invention relates to the inhibition of transforming growth
 XX factor-beta (TGF-beta) activity involving contacting TGF-beta with a
 XX purified polypeptide comprising leucine-rich amino acid sequence of a
 XX member of decorin superfamily of mammalian proteoglycans. The following
 XX activities can be attributed to the polypeptide of the invention:
 XX cyostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic,
 XX antiarteriosclerotic, hepatotropic, cardiant, dermatological and
 XX vulnerery. Polypeptides of the invention act as transforming growth
 XX factor-beta (TGF-beta) binder. The polypeptides of the invention can be
 XX used for treating a pathology, particularly proliferative pathology
 XX caused by a transforming growth factor-beta (TGF-beta) regulated
 XX activity such as cancer; particularly fibrotic cancer, fibrotic
 XX disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis,
 XX adult respiratory distress syndrome, cirrhosis of liver, fibrosis of
 XX lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty
 XX restenosis, renal interstitial fibrosis and certain dermal fibrotic
 XX conditions such as keloids and scarring resulting from burn injuries;
 XX other invasive skin injuries and reconstructive surgery. The wounds
 XX treated with the polypeptide, particularly decorin exhibit no detectable
 XX scarring, and are histologically normal. The current sequence represents
 XX human biglycan.

CC Sequence 368 AA;

CC Query Match 56.4%; Score 966; DB 22; Length 368;
 CC Best Local Similarity 56.5%; Pred. No. 2.9e-78;
 CC Matches 186; Conservative 51; Mismatches 90; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRFEPSLGPVCPFCOCHLRVQSGDLGDKVPPDPTLLDION 60
 DB 40 EASGADISGVLDPPSVPTTYGAMCPFGCHLRVQSCDLGKSPKXISDPTLLDION 99
 QY 61 NKTEIKDGFKNLKNLHLLIVNNKISKVSPGAFPLVKEKRLYSINQKELPEKPK 120
 DB 100 NDISLRKDDPKGQHLTALVYVNNKISKIKHKAFFSPRNQKLYISQNHVLEIPNLS 159
 QY 121 TLOELRAENETTKRKATFNGNLQMIYIEIGTNPLKSGIENGAFQMKKLSYRIADT 180

DB 160 SLEVLRIHNRIRKRVNGVSGLRNMCNMGPNLENSGFEPGAPDGL-KLNYLRISA 218

QY 181 NITSIPQGLPSPSTELHLDGKISRVDASLKGHNLAIGLSPNSISAVDNGSLANTPH 240
 DB 219 KLTGIPDLDLPTLNELHLDNKNLQALIELEDLKYSKLYRIGLGHQNRMLIENGSLSTLPT 278

QY 241 LREIHLNNKLTTRVPGSLAEHXYIQVYVYHNNNISVVGSSDPCPPGNTKASYSVSLF 300
 DB 279 LREIHLNNKLTARVPSGLPDLKLLQVYVYHNNNITKGVNDPCPMGFGVRAVYNGISLIF 338

QY 301 SNPYQWEIQSPTRCYVVSATOLGNYK 329
 DB 339 NNPPVWEVQPAIFRCVTDRLAIQFGNYK 367

RESULT 21

AA05159
 ID AA05159 standard; protein; 368 AA.
 XX AA05159;
 AC 25-MAR-2003 (updated)
 XX 17-DEC-2001 (updated)
 DT 09-OCT-1990 (first entry)

DE Sequence of human bone proteoglycan I (biglycan).
 XX Osteoporosis; rheumatoid arthritis; Paget's disease;
 XX atherosclerosis; periodontal; human bone matrix; proteoglycan.

XX Homo sapiens.
 XX USN7432044-N.
 XX 17-APR-1990.
 XX 03-NOV-1989; 89US-0142159.
 XX 03-NOV-1989; 89US-0142159.
 XX (USSH) NAT INST OF HEALTH.

XX Termino J;
 XX WPI; 1990-178641/23.
 XX N-BSDB; AA004490.

DR Human bone matrix DNA and proteins -
 PT used in detection, diagnosis and treatment involving skeletal
 XX and/or connective tissue disease states.

PS Disclosure; Page 7; ?pp; English.

CC Probes and Abs raised to the proteins can be used to determine
 CC their levels useful in diagnosis of associated connective tissue
 CC diseases states such as osteoporosis, osteo/rheumatoid arthritis,
 CC Paget's disease, arteriosclerosis and periodontal disease.
 CC Proteins may also be used to induce or block biological function.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NITS applications to prevent clauses with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/nits.html.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

CC Sequence 368 AA;

CC Query Match 56.3%; Score 965; DB 11; Length 368;
 CC Best Local Similarity 56.2%; Pred. No. 3.6e-78;
 CC Matches 185; Conservative 53; Mismatches 89; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRFEPSLGPVCPFCOCHLRVQSGDLGDKVPPDPTLLDION 60

Db 40 BASGADTSGVLDPDSVTPTYSAMCPFGCHLRVVOCSDLGLKSVPEISPDITLLDLQN 99
 QY 61 NKITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 120
 Db 100 NDISLAKDPKFGKQHLVAVLVNNKISKIHEKAFSPLRNQLKYLISGNHVEIPMLPS 159
 QY 121 TLOELRAHENEITVRKKTENGMLNOMIVIELGTNPLKSSGGENGAFQGMKCLSTIRIADT 180
 Db 160 SLVAVRITHDNIRKRVKGVSPFGLRNMCIEWGNPLESGFEPGAFGL-CLNLTARISA 218
 QY 181 NITSIPQGLPSELTHLDGKISRVDASLKGNNLAKGLSPNSISAVDNGSLAMTPH 240
 Db 219 KLTGIPDLPETLWELHLDHKKIQALIELEDLRYSKYLRLGHNQIMTEGSLFLPT 278
 QY 241 LREIHLNNKLTVPVPGGLAEHKYIQVYLNHNNNISVVGSSDFCPGHNTKASYSVSLF 300
 Db 279 LREIHLNNKLTARVPSGLPDLKLIQVYVYLNHNNITKGVNDPCMGFEGVKAAYNGISLF 338
 QY 301 SNPVQWEIQPSTFCVYVRSALIQGNK 329
 Db 339 NNVPVWEVGPATFRCVTDRLAIQFGNYK 367

RESULT 22

AA042264 standard; Protein; 186 AA.

AA042264;

25-MAR-2003 (updated)
 09-JAN-2003 (updated)
 DT 28-APR-1994 (first entry)

Decorin sequence PT-75 (N-terminal to LRR6).

leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
 fusion protein; maltose binding protein; tumour growth; inhibition;
 decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.

Bos sp.

WO9320202-A1.

14-OCT-1993.

02-APR-1993; 93WO-US03171.

03-APR-1992; 92US-0865652.

(LJOL-) LA JOLLA CANCER RES FOUND.

Cardenas J, Craig W, Mullen DG, Pierschbacher MD;

Ruoslahti E;

WPI; 1993-336910/42.

N-PSDB; AA050050.

Active fragments of protein esp. decorin - with cell regulatory
 factor domain, useful for inhibiting cell regulatory factor
 activity

Claim 10; Page 43-44; 77p; English.

Active fragments of decorin (full-length coding sequence AA050046)

were generated by PCR and fused to Maltose Binding Protein. The

resulting fusion proteins were useful for inhibiting the activity of

a cell regulatory factor, esp. TGF-beta, and hence for treating

conditions associated with over-activity of the growth factor such

as certain tumours.
 (Updated on 09-JAN-2003 to add missing OS field.)
 (Updated on 25-MAR-2003 to correct PN field.)
 Sequence 186 AA;

Query Match 55.3%; Score 948; DB 14; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4, 5e-77;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDPDPFSLQPVCPFCQCHLRVVOCSDLGLDKVPKDLPEDTLLDLQN 61
 Db 4 EASGIGPEVDDPDPFSLQPVCPFCQCHLRVVOCSDLGLDKVPKDLPEDTLLDLQN 63
 QY 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 121
 Db 64 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 123
 QY 122 LOELRAHENEITVRKKTENGMLNOMIVIELGTNPLKSSGGENGAFQGMKCLSTIRIADT 181
 Db 124 LOELRAHENEITVRKKTENGMLNOMIVIELGTNPLKSSGGENGAFQGMKCLSTIRIADT 183
 QY 182 ITS 184
 Db 184 ITS 186

RESULT 23

AA01311 standard; Protein; 379 AA.

AA01311;

25-SEP-2000 (first entry)

Human PRO241 polypeptide.

PRO; membrane bound protein; secreted protein; PRO357; PRO327;
 PRO243; PRO715; PRO241; PRO323; PRO299; PRO344; PRO347;
 PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 antibody; screening; detection; inhibition; probe; primer; human.

Homo sapiens.

OS XX

PH XX

Key Peptide

Location/Qualifiers
 1..15
 /label= Signal peptide

Modified-site 129..135
 /note= "N-myristoylation site"

Domain 154..176
 /label= Leucine zipper pattern

Modified-site 210..216
 /note= "N-myristoylation site"

Modified-site 214..220
 /note= "N-myristoylation site"

Modified-site 237..243
 /note= "N-myristoylation site"

Modified-site 270..276
 /note= "N-myristoylation site"

Modified-site 281..285
 /note= "N-glycosylation site"

Modified-site 282..288
 /note= "N-myristoylation site"

WO200032776-A2.

08-JUN-2000.

01-DEC-1999; 99WO-US26301.

01-DEC-1998; 98WO-US25108.

16-DEC-1998; 98US-0112850.

22-DEC-1998; 98US-0113296.

(GETH) GENENTECH INC.

PI Baker KP, Boetstein D, Eaton DL, Ferrara N, Filvaroff E,
 PI Geritseen ME, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL,
 PI Hillan KJ, Kijavini IU, Napier MA, Roy MA, Tumas D, Wood WI;
 DR WPI; 2000-412324/35.
 DR N-PSDB; AAA49551.
 XX
 PT New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 PS
 PS Claim 12; Fig 2; 187pp; English.
 CC
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 CC
 SQ Sequence 379 AA;
 Query Match 55.1%; Score 943.5; DB 21; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 Oy 11 PDDRDPEPGLGVPCCCHLRVQCSPLGDKVKDLPPTTLIDLNKKITTEKDD 70
 Db 61 PSHHFPPLPFMCPEGCGCCYSRVHCSDLGLTSVTNIPDTRMDLONNKIKELKEND 120
 Oy 71 FNNLNALILVNNKISVSPGAFPLVLEKLYLKNQKLPKPKMKTLOELRAHN 130
 Db 121 FGLGSLVGLILNNKLTLPKPAFLTKKRLVLYSHNQSLPILNKLAEIRHN 180
 Oy 131 ETTXKRTKFNGLNQIVLELGNPLKSGIERGACQKKLSYRIADNTITSIPGCP 190
 Db 181 KVKKKIQKDTFKGMNLAHLVEMSNAPLDNNGISPGAEVGVTVFHIRIAEAKLTSVPKGLP 239
 Oy 191 PELTEHLADGNKISRDAASLKGNNLALGLSFNSISAVDNGSLANTPEHLHDDNK 250
 Db 240 PTLLEHLADYNKISTYLEDFPKYKQLQKLGANNKITIENSLNITRVEHLNNK 299
 Oy 251 LTRVPGGLAEHKYIQVYVLLHNNNISVYSSDPFCPEHNTKASYSVSLSPNPVQYMEIO 310
 Db 300 LKKIPGGLPELKYLIITIFLHNSIARVGVNDFCTVPRKMKSLYSLSLFPNPKYKMEIO 359
 Oy 311 PSTFRGVYRSALQLGNY 328
 Db 360 PATFRCVLSRMSVOLGNF 377
 RESULT 24
 AAU12335
 ID AAU12335 standard; Protein; 379 AA.
 AC AAU12335;
 DT 24-OCT-2001 (first entry)
 XX
 XX Human PRO241 polypeptide sequence.
 DE
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.

XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritseen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-408281/43.
 DR N-PSDB; AAS21407.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 PS
 PS Claim 12; Fig 328; 813pp; English.
 XX
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 379 AA;
 Query Match 55.1%; Score 943.5; DB 22; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

QY 11 PDDRDPEPSLGPVCPFCQCHLRVVOCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGD 70
DB 61 PRSHFFPFDLPFMCPCFCQCYSRVHCSDDLGLTSVPTNIPFDTMLDLONNKIKEIKEND 120
QY 71 FKNLKNLHALILVNKKISKVSPGAFPLVLELYLSKNQKELPEKMPKTLIOELRAHEN 130
DB 121 FKGLTSLYGLILNNKLTIKHPKAFLLTKKRLYLISHNQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKVTENGILNOMIVIELGTPPLKSSGIENGAFQGMKKLSYIRIADTNTITSIPQGLP 190
DB 181 KVKKIQKOTFKGMALHVLHMSANPLDNNNGIEPGAEGEV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSTLELHDGKISRVDASLKGILNLAAGLGSFNSISAVDNGSLANTPHLREHLDDNNK 250
DB 240 PTLLELHLDYKNTLVELEDFRKYKELQRLGLGNKKITDIENGSLANIPRAEIHLENNK 299
QY 251 LTRVPGGLAEHKYQIVVYLLNNNISVVGSSDFPCPGHNTKASYSVGLFSNPVQYWEIQ 310
DB 300 LKKTIPSGLPKLYLOITFLHNSIARVGVNDPCFTVPKMKSLYSALSLFNNPVKYMWO 359
QY 311 PSTFRCVYVRSALQIGNTY 328
DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 25
ABB95437
ID ABB95437 standard; Protein; 379 AA.
XX
AC ABB95437;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO241 SEQ ID NO: 30.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiatic; cytosclastic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
XX
PR 25-JUL-2000; 2000US-220634P.
XX
PR 25-JUL-2000; 2000US-220664P.
XX
PR 28-JUL-2000; 2000WO-US20710.
XX
PR 02-AUG-2000; 2000US-222695P.
XX
PR 17-AUG-2000; 2000US-0643657.
XX
PR 23-AUG-2000; 2000WO-US23552.
XX
PR 24-AUG-2000; 2000WO-US23358.
XX
PR 07-SEP-2000; 2000US-230978P.
XX
PR 15-SEP-2000; 2000US-000000P.
XX
PR 18-SEP-2000; 2000US-0664610.
XX
PR 18-SEP-2000; 2000US-0665350.
XX
PR 24-OCT-2000; 2000US-242922P.
XX
PR 08-NOV-2000; 2000US-0709238.
XX
PR 08-NOV-2000; 2000WO-US30932.
XX
PR 10-NOV-2000; 2000WO-US30873.
XX
PR 01-DEC-2000; 2000WO-US32678.
XX
PR 20-DEC-2000; 2000US-0747259.
XX
PR 20-DEC-2000; 2000WO-US34956.
XX
PR 22-JAN-2001; 2001US-0767609.
XX
PR 28-FEB-2001; 2001US-0796498.
XX
PR 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2001; 2001WO-US06666.
XX
PR 09-MAR-2001; 2001US-0802706.

```

```

PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GERTH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERB) FERRARA N.
PA (GERB) GERBER H.
PA (GERB) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
PI WPI; 2002-171999/22.
XX
DR N-PSDB; ABL95575.
XX
DE One hundred and eighty seven nucleic acids encoding PRO polypeptides,
DE useful in diagnosis and treatment of cardiovascular (e.g. myocardial
DE infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 30; 567bp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 379 AA;
XX
Query Match 55.1%; Score 943.5; DB 23; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRDPEPSLGPVCPFCQCHLRVVOCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGD 70
DB 61 PRSHFFPFDLPFMCPCFCQCYSRVHCSDDLGLTSVPTNIPFDTMLDLONNKIKEIKEND 120
QY 71 FKNLKNLHALILVNKKISKVSPGAFPLVLELYLSKNQKELPEKMPKTLIOELRAHEN 130
DB 121 FKGLTSLYGLILNNKLTIKHPKAFLLTKKRLYLISHNQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKVTENGILNOMIVIELGTPPLKSSGIENGAFQGMKKLSYIRIADTNTITSIPQGLP 190
DB 181 KVKKIQKOTFKGMALHVLHMSANPLDNNNGIEPGAEGEV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSTLELHDGKISRVDASLKGILNLAAGLGSFNSISAVDNGSLANTPHLREHLDDNNK 250

```


KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytostatic.
 XX Homo sapiens.
 OS US2003036180-A1.
 XX
 XX 20-FEB-2003.
 PD
 XX
 PF 09-MAY-2002; 2002US-0143114.
 XX
 XX 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 17-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22391.
 PR 29-OCT-1998; 98WO-US22392.
 PR 29-OCT-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US10733.
 PR 14-MAY-1999; 99WO-US12252.
 PR 02-JUN-1999; 99WO-US20111.
 PR 01-SEP-1999; 99WO-US20594.
 PR 08-SEP-1999; 99WO-US20944.
 PR 13-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 15-SEP-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 22-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US34956.
 PR 20-DEC-2000; 2000WO-US3678.
 PR 26-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 16-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR N-PSDB; ACA03766.
 XX
 XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 XX Claim 12; Fig 328; 660pp; English.
 PS
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA. In the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB06570-AB06684 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at

CC segdata.uspto.gov/psipdbIdentEntry.html.
XX Sequence 379 AA;
SQ
Query Match 55.1%; Score 943.5; DB 24; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRFEPSLGFVCPFCQCHLRVQCSDLGLKVPKDI.PPPTTLIDLQNNKITEIKOD 70
DB 61 PRSHFFPFDLPFMCPEFGCCGSRVHCSDLGLTSVPNTIPFPTRMIDLQNNKIKIKEND 120
QY 71 ENLKNLHLLIIVNNKISKVSGAFTPLVKEELRTISKQKELPEKPKTLOELPAHEN 130
DB 121 FGLTSLGLILNNKLTIKHPKFLTTKLRRLYSNHQLSIEIPLNLPKSLAEIRIHEN 180
QY 131 EITVKRVKVPFNGIANQIVIEELGNPLKSSGIENGAFQGGKLSYRIADNTNTSIPOGLP 190
DB 181 KVKKIQKOTPKGMNLAHVEMANPLDNGIEFGAFEGV-TVFHRIAKLTSPKGLP 239
QY 191 PELTEIHLIDGNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTEPHLRLHDNNK 250
DB 240 PELTEIHLIDYNNKISTVELEDPRKYELOELGLGNKKITDIENGSLANIPIVAEIHLENNK 299
QY 251 LTRVGGLAHEKTYIQVVIHANNISVSGSDPCPGHNTKKASYSVGSLSFNPVOYWEIO 310
DB 300 LKRTISGLPELKYLDIIFLHNSIARVGNDCPTVPKMKSLYSALISFNNPVKXWEMQ 359
QY 311 PSTFCVYVRSALIQGNV 328
DB 360 PATFRCVLSRMSVQLGNF 377
RESULT 28
ABU67009
ID ABU67009 standard; Protein; 379 AA.
XX AC ABU67009;
XX DT 27-MAY-2003 (first entry)
XX DE Human secreted/transmembrane, PRO, protein SEQ ID 328.
XX KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX OS Homo sapiens.
XX PN US2003032155-A1.
XX PD 13-FEB-2003.
XX PF 03-MAY-2002; 2002US-0137865.
XX PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05009.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US07532.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30973.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US27259.
PR 28-FEB-2001; 2001US-079648.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.

PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-331925/31.
XX
XX N-PSDB; ACA04187.
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX
XX Claim 12; Fig 328; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
XX at least 80% identical to, or the full-length coding sequence of, any of
XX the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
XX (one of 275 secreted or transmembrane proteins). The nucleic acid
XX further comprises the full-length coding sequence of the DNA deposited
XX under American Type Culture Collection (ATCC) accession number in a list
XX given in the specification. Also included are vectors and host
XX cells for producing PRO proteins, PRO fusion proteins, anti-PRO
XX antibodies, PRO extracellular domains and mature sequences, methods
XX of detecting PRO proteins, methods for stimulating the release of
XX TNF-alpha (tumour necrosis factor alpha) from human blood,
XX (and the proliferation of differentiation of chondrocyte cells, the
XX proliferation of, or gene expression in pericyte cells, the release or
XX proteoglycans from cartilage, proliferation of inner ear utricular
XX supporting cells, the proliferation of T-lymphocyte cells, the release
XX of a cytokine from peripheral blood mononuclear cells (PBMC), or the
XX proliferation of endothelial cells), a method for modulating the uptake
XX of glucose or free fatty acid (FFA) by skeletal muscle cells,
XX a method for inhibiting the binding of A-peptide to factor VIIa,
XX or the differentiation of adipocyte cells, a method for detecting the
XX presence of a tumour in a mammal and an oligonucleotide probe derived
XX from any of the nucleotide sequences cited above. The nucleic acids and
XX polypeptides are useful for treating inflammatory diseases, organ
XX failure, atherosclerosis, cardiac injury, infertility, birth defects,
XX premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
XX diabetic complications. The nucleic acids are useful as hybridisation
XX probes, in chromosome and gene mapping, and in generating antisense RNA
XX or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
XX biosensors or bioreactors. Both are useful in tissue typing.
XX The present sequence represents a PRO protein of the invention.
XX
XX Sequence 379 AA;
SQ
Query Match 55.1%; Score 943.5; DB 24; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRDPEPSLGVPCPRCCCHLRVQCSLGLDKVPKDI.PPTTLADLONNKITEIKXOD 70
DB 61 PRSHFPFPLPMPCCPGCCQCYSVVHCSLGLTSVPTNIPFTRMDLONNKIKEXKEND 120
QY 71 PKNLKLHLLIYNNKISKVSPAFPLVYKLELYLSKQKLELPEKMKPTQELFAHN 130
DB 121 FKGLTSLYGLILNNNKLTHPPAFLLTKKLRLYLSHQSLSTIPNLPSLAELIHEN 180
QY 131 ELTKVAKTFNGNLQMIIVIELGTNPSSGIEGAFQGMKKLSYIRIADTNITSIDQGLP 190

DB 181 KVKKIQKDPFKGNALHLEMSANPLDNNGIEPGAEV-TVPHIRIAEKLTSVPGGLP 229
QY 191 PSTLEHLIDGNKISRVDASLKGILNLIAGLSFNSISAVDNGSLANTPHLREHLDNKK 250
DB 240 PTLLEHLIDNKKSTYELBEFKYKELQRLGLNKKITDLENSLNI PVRREHLNKK 299
QY 251 LTRVPGGLAEKHYIQVYLIHNNNI SVVGSDFPCPPGHNTKKASVGLFSNPQVWEIQ 310
DB 300 LKKIPSGLPKLTQLTIFLHNSIARVGVDFCPTVPKMKKSLYSALISLFPNPKWEMQ 359
QY 311 PSTPRCYVNSAIOLENY 328
DB 360 PATFRCLSRMSVQLGNF 377
RESULT 29
ABU67121
ID ABU67121 standard; Protein; 379 AA.
XX
XX ABU67121;
AC
XX
XX 27-MAY-2003 (first entry)
DT
XX
XX Human PRO polypeptide #1.
DE
XX
XX Human; PRO; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; neural damage; trauma; inflammatory disease; AIDS;
KW chemotherapy; organ failure; atherosclerosis; cardiac injury; diabetes;
KW infertility; birth defect; premature aging; tumour; wound healing;
KW cancer; neoplastic; neuroprotective; anti-HIV; antidiabetic; cardiac;
KW antiatherosclerotic; antiinflammatory; antiparkinsonian; cytostatic;
KW antiinfertility; vulnerary.
XX
XX
XX Homo sapiens.
OS
XX
XX US2002165143-A1.
PN
XX
XX 07-NOV-2002.
PD
XX
XX 30-AUG-2001; 2001US-0944403.
PF
XX
XX 16-SEP-1998; 98WO-US19330.
PR 01-DEC-1998; 98WO-US25108.
XX 22-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
XX 22-FEB-2000; 2000WO-US03665.
PR 11-FEB-2000; 2000WO-US04414.
XX 02-MAR-2000; 2000WO-US05841.
PR 30-MAR-2000; 2000WO-US08439.
XX 22-MAY-2000; 2000WO-US14042.
PR 28-JUL-2000; 2000WO-US20710.
XX 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
XX 03-DEC-1997; 97US-067411P.
PR 11-DEC-1997; 97US-069278P.
XX 11-DEC-1997; 97US-069334P.
PR 12-DEC-1997; 97US-069335P.
XX 12-DEC-1997; 97US-069425P.
PR 16-DEC-1997; 97US-069694P.
XX 16-DEC-1997; 97US-069696P.
PR 16-DEC-1997; 97US-069702P.
XX 17-DEC-1997; 97US-069870P.
PR 17-DEC-1997; 97US-069873P.
XX 18-DEC-1997; 97US-068017P.
PR 05-JAN-1998; 98US-070440P.
XX 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
XX 25-FEB-1998; 98US-075945P.

PR 16-DEC-1998; 98US-112850P.
PR 22-DEC-1998; 98US-113296P.
PR 28-JUL-1999; 99US-146222P.
PR 25-MAY-2001; 2001US-086602B.
PR

(GETH) GENENTECH INC.

Baker KP, Bobcotein D, Eaton DL, Ferrara N, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IU, Napier MA, Roy MA, Tumas D, Wood WI;

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease -

Claim 12; Fig 2; 171pp; English.

The invention relates to an isolated human PRO polypeptide and the PRO polypeptide encoding it. The PRO polypeptides and nucleic acids are useful in diagnosing or treating neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, and neural damage, e.g. due to trauma or after chemotherapy, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, diabetic complications and mutations in general. The polypeptides are useful for diagnosing tumours, or for inhibiting the growth of tumour cells. The polypeptides are also useful for wound healing and associated therapies concerned with re-growth of tissue. The polynucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reactions, and to generate transgenic or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents for chromosome identification and tissue typing. The PRO sequences are also useful in gene therapy and as molecular weight markers for protein electrophoresis purposes. Sequences ABU67121-ABU67136 represent human PRO polypeptides of the invention.

SQ Sequence 379 AA;

Query Match	55.1%;	Score 943.5;	DB 24;	Length 379;
Best Local Similarity	55.0%;	Pred. No. 3.2e-76;		
Matches 175;	Conservative 60;	Mismatches 82;	Indels 1;	Gaps 1

Qy	1	PDDRPFPSLGPVCPRCOCHLRVYOCSDLGDXPKDPRDPTLLDYONNKITEIDGD	70
Db	61	PRSHFPPDFPMPCCPCCOCSRVHCHSDGLTSVPTNIPDTRMLDQNNKIKEIEND	120
Qy	71	FKOLKJLHALLVNNKISKVSFGAFTPLVKLERLYLSHNOUKELPERKMPKTLQELRAHEN	130
Db	121	FKGLTSLYGLILNNKLTTHHPKAFETTKGLERLISHNOUSRIPLNPKSLAELRIHEN	180
Qy	131	EITKVRKRVFNENGLNOMIVIELGNPLKSGGIEENGAFQOAKKLTSTYRLADNTITSIPGGLP	190
Db	181	KWKIKQKOTPKKNNALHVLGEMANPLDNNGIEPQAFBGV-TVFHIRLAEALTSVPGGLP	239
Qy	191	PSLTELHLDGNTKISRVAASLKGJLNNLAKLGSLFNSISAVDNGSIANTPHLREHLADNNK	250
Db	240	PTLLELHLLYNNKISTVELEDFRKYKLEQRLGJGNNKIIDIEENGSIANIPRVREIHLNNK	299
Qy	251	LTVFPGGLAEHKIIOVVYLLHNNNISVSGSDPCPBGHNTTKKASVGSUSJBNPOVWEIO	310
Db	300	LKKIPBSGLPELKLQIIFLHNSIARVGVNDFCTVPKOKSLYSALSFLNNPKYWEQO	359
Qy	311	PSFTRCYVRSALQIGNY	328
Db	360	PATFRCYLSRMSVOLGNF	377

	RESULT 30	
ABUS9814	ABUS9814 standard; Protein; 379 AA.	
ID	ABUS9814	
AC	ABUS9814;	
XX		
DT	13-MAY-2003 (first entry)	
XX		
DE	Novel secreted and transmembrane protein PRO241.	
XX		
KM	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing	
KM	cardiac insufficiency disorder; cancer; tumour; immune response;	
KM	adrenal cortical capillary endothelial growth; c-fos induction;	
KM	vascular endothelial growth factor inhibition; VEGF inhibition;	
KM	endothelial cell growth inhibitor; T-lymphocytes stimulation;	
KM	retinal neurons cell survival; rod photoreceptor cell survival;	
KM	retinal disorder; retinitis pigmentosa; kidney disease;	
KM	mammalian kidney mesangial cell proliferation; Berger disease;	
KM	dematitis; herpetiformis; Crohn's disease; chondrocyte proliferation;	
XX	chondrocyte redifferentiation; sports injury; arthritis.	
XX		
OS	Homo sapiens.	
PN	US2003017563-A1.	
XX		
PD	23-JAN-2003.	
XX		
PF	07-MAY-2002; 2002US-0140808.	
XX		
PR	31-MAR-1997; 97WO-US05230.	
PR	12-JUN-1998; 98WO-US12456.	
PR	14-JUL-1998; 98WO-US14552.	
PR	28-AUG-1998; 98WO-US17888.	
PR	10-SEP-1998; 98WO-US18824.	
PR	14-SEP-1998; 98WO-US19093.	
PR	14-SEP-1998; 98WO-US19092.	
PR	14-SEP-1998; 98WO-US19177.	
PR	16-SEP-1998; 98WO-US19330.	
PR	17-SEP-1998; 98WO-US19437.	
PR	07-OCT-1998; 98WO-US21141.	
PR	29-OCT-1998; 98WO-US22991.	
PR	29-OCT-1998; 98WO-US22992.	
PR	20-NOV-1998; 98WO-US24855.	
PR	01-DEC-1998; 98WO-US25108.	
PR	05-JAN-1999; 99WO-US00106.	
PR	08-MAR-1999; 99WO-US05028.	
PR	10-MAR-1999; 99WO-US05190.	
PR	20-APR-1999; 99WO-US08615.	
PR	14-MAY-1999; 99WO-US10733.	
PR	02-JUN-1999; 99WO-US12252.	
PR	01-SEP-1999; 99WO-US20111.	
PR	08-SEP-1999; 99WO-US20594.	
PR	13-SEP-1999; 99WO-US20944.	
PR	15-SEP-1999; 99WO-US21090.	
PR	15-SEP-1999; 99WO-US21547.	
PR	05-OCT-1999; 99WO-US23089.	
PR	29-NOV-1999; 99WO-US28214.	
PR	30-NOV-1999; 99WO-US28313.	
PR	01-DEC-1999; 99WO-US28309.	
PR	01-DEC-1999; 99WO-US28301.	
PR	01-DEC-1999; 99WO-US28634.	
PR	02-DEC-1999; 99WO-US28551.	
PR	02-DEC-1999; 99WO-US28564.	
PR	02-DEC-1999; 99WO-US28565.	
PR	16-DEC-1999; 99WO-US30095.	
PR	20-DEC-1999; 99WO-US30911.	
PR	20-DEC-1999; 99WO-US30999.	
PR	22-DEC-1999; 99WO-US30720.	
PR	30-DEC-1999; 99WO-US31243.	
PR	30-DEC-1999; 99WO-US31274.	
PR	05-JAN-2000; 2000WO-US00219.	
PR	06-JAN-2000; 2000WO-US00277.	
PR	06-JAN-2000; 2000WO-US00376.	

PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 20-MAR-2000; 2000WO-US06884.
 PR 21-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX MPI, 2003-148238/14.
 DR N-PSDB; ABX89304.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments
 XX
 PS Claim 12, Fig 328; 659pp; English.
 CC The invention describes an isolated human PRO polypeptide. The PRO

CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO526,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1346 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiforms or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.

XX Sequence 379 AA;

Query Match 55.1%; Score 943.5; DB 24; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRPEPSIGVPCPPFCQCHLRVQCSDGLGKVPKDLPPDTLLDQNNKITEIKDGD 70
 DB 61 PRSHFPFPPDLFPKCPFCQCQCSRVHCSIDLGTSVPTNPIDPTMLDQNNKIKEIKEND 120
 QY 71 FQNLKNTAHLLVNNKISKVSPGAFPLVVKLERLYLKNOLKELPEKPKTLOELRAHEN 130
 DB 121 FKGITSLYGLLNNKNTKTHPKAFVTTKCKRRYLSHNSLPLNPKSLAEIRIHEN 180
 QY 131 EITVRKYVTENGILQMTVIEIGTNPDKSSGIENGAFQGMKLSYRIADTNITSIPQGLP 190
 DB 181 KVKKIQKDTFKGNALVLEMSANPLDNNGIEPAFEGV-TVFHIRIAEALTSVPKGLP 239
 QY 191 PSLTELDHGNKISRVDASIKGINLAKTGLSNSISIAVNGSLANTPHIRELHLDNNK 250
 DB 240 PTLLELDHYNKISTVELDFKRYKELQRLGLGNKKITDIENGSLANIPVREHLLENK 299
 QY 251 LTRVPGGLAEHKYQVYVYLLHNNISVYSGSDPFCPGHNTKKASYLSFNPQWYEIQ 310
 DB 300 LKKIPSGLPKELKYQIIFLSHNSIARVGVNDPCTVPKMKLSYSAISLFNNPKWEMQ 359
 QY 311 PSTFRCVYVRSALIQAGNY 328
 DB 360 PATFRCLSRMSVQLGNP 377

Search completed: February 9, 2004, 11:35:56
 Job time : 81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 11:21:34 ; Search time 38 seconds

(without alignments)
832.618 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713
Sequence: 1 VEASGIGPEVDDRDPEPSL.....QPSTFCVYVSAIQGNVYK 329

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1709	99.8	359	1	NEHUC8
2	1564.5	91.3	360	2	S06280
3	1564.5	91.3	360	2	I47020
4	1415	82.6	357	2	S24317
5	1365.5	79.7	354	2	A55454
6	1331.5	77.7	354	2	S29145
7	985.5	57.5	369	2	S32793
8	984.5	57.5	369	2	S20811
9	982.5	57.4	369	2	S32559
10	979	57.2	368	1	BGHUN
11	385.5	22.5	382	2	I39068
12	365.5	21.3	343	2	A41748
13	365.5	20.8	342	2	A46743
14	347.5	19.3	338	2	S52284
15	327.5	19.1	1531	2	T42218
16	327	19.1	1523	2	T13953
17	326.5	19.1	376	2	S55275
18	323	18.9	1469	2	B36665
19	323	18.9	1480	2	A36665
20	314.5	18.4	375	2	S05390
21	314	18.3	1025	2	T42626
22	298.5	17.4	380	2	S71876
23	295.5	17.3	907	2	J60176
24	293	17.1	361	2	A53860
25	291	17.0	1091	2	A58532
26	285.5	16.7	907	2	UG0193
27	283.5	16.5	707	2	JC7763
28	273	15.9	605	2	JC5239
29	273	15.9	605	2	A41915

30	272	15.9	603	2	JC1282	insulin-like growth
31	264.5	15.4	603	2	JC6128	insulin-like growth
32	261	15.2	680	2	T19939	hypothetical prote
33	254	14.8	316	2	A41781	proteoglycan-Ib -
34	252.5	14.7	322	2	S72271	proteoglycan-Lb pr
35	248.5	14.5	536	2	A34901	lysine carboxypept
36	246.5	14.4	1389	2	T13852	gene wheeler prote
37	244	14.2	738	2	T13857	hypothetical prote
38	240.5	14.0	1385	2	T13887	tilr protein - frui
39	238	13.9	298	2	JC4130	osteoglycin precu
40	236.5	13.8	560	2	A60164	platelet membrane
41	233	13.6	594	2	T23841	hypothetical prote
42	231.5	13.5	333	2	T34555	hypothetical prote
43	231.5	13.5	662	2	S42799	garp precursor - h
44	231	13.5	610	2	T23836	hypothetical prote
45	226	13.2	2493	2	A55481	adenylate cyclase

ALIGNMENTS

RESULT 1

NEHUC8

decorin precursor - human

N:Alternate names: cartilage proteoglycan protein II; DS-Pg II; PG40 core protein; pr

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 21-Jan-2000

C:Accession: A45016; A45015; B45015; A26476; S06640

R:Vetter, U.; Vogel, W.; Jue, W.; Young, M.F.; Fisher, L.W.

Genomics 15, 161-168, 1993

A:Title: Human decorin gene: intron-exon junctions and chromosomal localization.

A:Reference number: A45016; MUID:93162643; PMID:8432527

A:Accession: A45016

A:Molecule type: DNA

A:Residues: 1-359 <VER>

A:Cross-references: GB:L01125; GB:L01126; GB:L01127; GB:L01128; GB:L01129; GB:L01130;

A:Note: sequence extracted from NCBI backbone (NCBIP:125061)

R:Danielson, K.G.; Fazio, A.; Cohen, I.; Cannizzaro, L.A.; Blacheteter, I.; Iozzo, F

Genomics 15, 146-160, 1993

A:Title: The human decorin gene: intron-exon organization, discovery of two alternati

A:Reference number: A45015; MUID:93162642; PMID:8432526

A:Accession: A45015

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 28-70 <DA2>

A:Cross-references: GB:M98262

A:Note: sequence extracted from NCBI backbone (NCBIP:125013)

A:Accession: B45015

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 236-359 <DAN>

A:Note: sequence extracted from NCBI backbone (NCBIP:125017)

R:Krusius, T.; Ruoslahti, E.

Proc. Natl. Acad. Sci. U.S.A. 83, 7683-7687, 1986

A:Title: Primary structure of an extracellular matrix proteoglycan core protein deduc

A:Reference number: A26476; MUID:87017013; PMID:3484330

A:Accession: A26476

A:Molecule type: mRNA

A:Residues: 1-359 <KRU>

A:Cross-references: GB:M14219; NID:G181169; PIDN:AA800774.1; PID:G181170

R:Broughley, P.J.; White, R.J.

Biochem. J. 262, 823-827, 1989

A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties

A:Reference number: S05639; MUID:90073579; PMID:2590169

A:Accession: S05640

A:Molecule type: protein

A:Residues: 31-33, 'X', 35-50 <ROU>

C:Comment: This protein binds type I collagen.

C:Genetics:

A:Gene: GDB:DCN

A:Cross-references: GDB:119839; OMIM:125255

A:Map position: 12q21.3-12q23

A:introns: 71/1; 108/3; 180/1; 218/1; 249/2; 295/3

A>Note: the first two introns occur before the initiator codon
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C:Keywords: Chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; dupli
F:1-16/Domains: signal sequence #status predicted <SIG>
F:17-30/Domains: propeptide #status predicted <PRO>
F:31-359/Product: decorin #status predicted <MPT>
F:48-72/Domains: proteoglycan amino-terminal homology <PAH>
F:82-105/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:106-129/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:130-150/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:151-174/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:175-200/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:201-221/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:222-245/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:246-269/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:270-292/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:293-316/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:308-359/Domains: proteoglycan carboxyl-terminal homology <PCH>
F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
F:189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F:211,262,303/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 1709; DB 1; Length 359;
Best Local Similarity 100.0%; Pred No. 9, 5e-118;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGPVCPFCQCHLRVVCSDGLDKVPDLPPDTLLDLDQNN 61
DB 32 EASGIGPEVDDRDPEPSLGPVCPFCQCHLRVVCSDGLDKVPDLPPDTLLDLDQNN 91
QY 62 KITEIKDGPFKNLKNIHALILVNNKISKYSPGAFPLVLYLERLYLSKNOLKEIPKMPKT 121
DB 92 KITEIKDGPFKNLKNIHALILVNNKISKYSPGAFPLVLYLERLYLSKNOLKEIPKMPKT 151
QY 122 LOELRAHEHETKVRKVTENGKLNQMVIELGTNPLKSSGIGENAFQGMKLSYIRADNN 181
DB 152 LOELRAHEHETKVRKVTENGKLNQMVIELGTNPLKSSGIGENAFQGMKLSYIRADNN 211
QY 182 ITSIPQGLPPLSTELHLDGKLSRVDAASIKGLNNAKLGLSFNSISAVDNGSLANTPHL 241
DB 212 ITSIPQGLPPLSTELHLDGKLSRVDAASIKGLNNAKLGLSFNSISAVDNGSLANTPHL 271
QY 242 REHLHDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKASYSVGLS 301
DB 272 REHLHDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKASYSVGLS 331
QY 302 NPQVWEIOPSTRCYVVSATQLGNKY 329
DB 332 NPQVWEIOPSTRCYVVSATQLGNKY 359

RESULT 2

S06280
decorin precursor - bovine
N:Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 20-Aug-1999
C:Accession: S06280; B31430; A26545; A20935
R:Day, A.A.; McQuillan, C.I.; Termine, J.D.; Young, M.R.
Biochem. J. 248, 801-805, 1987
A:Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan II
A:Reference number: S06280; MID:88133946; PMID:3435485
A:Accession: S06280
A:Molecule type: mRNA
A:Residues: 1-360 <DAY>
A:Cross-references: EMBL:Y00712; NID:g618; PIDD:CAA6702.1; PID:g619
A:Experimental source: bone
R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
J. Biol. Chem. 264, 2876-2884, 1989
A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, fro
A:Reference number: A31430; MID:89123388; PMID:2914936
A:Accession: B31430
A:Molecule type: protein

A:Residues: 31-33, 'X', 35-54 <CHO>
A:Experimental source: cartilage; fetal skin
R:Coester, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.
J. Biol. Chem. 262, 3809-3812, 1987
A:Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t
A:Reference number: A26545; MID:87137687; PMID:3818667

A:Accession: A26545
A:Molecule type: protein
A:Residues: 31-50 <COS>
A:Experimental source: sclera
R:Pearson, C.H.; Wintrob, N.; Packre, D.S.; Scott, P.G.; Carpenter, M.R.
J. Biol. Chem. 258, 15101-15104, 1983
A:Reference number: A20935; MID:84087911; PMID:6654908
A:Accession: A20935
A:Molecule type: protein
A:Residues: 31-54 <PEA>

A:Experimental source: skin
R:Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Packre, D.S.; Scott, P.G.
Biochem. J. 232, 277-279, 1985
A:Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulpi
nces around glycosylation sites in different proteoglycans.
A:Reference number: A44700; MID:86103195; PMID:3936484

A:Contents: annotation; glycosylation
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
C:Keywords: Chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext
F:1-15/Domains: signal sequence #status predicted <SIG>
F:16-30/Domains: propeptide #status predicted <PRO>
F:31-360/Product: decorin #status predicted <MPT>
F:49-73/Domains: proteoglycan amino-terminal homology <PAH>
F:83-106/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:107-130/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:131-151/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:152-175/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:176-199/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:202-222/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:223-246/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:247-270/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:271-293/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:294-308/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:309-360/Domains: proteoglycan carboxyl-terminal homology <PCH>
F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
F:190,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F:212,263,304/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.3%; Score 1564.5; DB 2; Length 360;
Best Local Similarity 89.7%; Pred No. 3, 7e-107;
Matches 296; Conservative 19; Mismatches 12; Indels 3; Gaps 2;

QY 2 EASGIGPE--VDDRDPEPSLGPVCPFCQCHLRVVCSDGLDKVPDLPPDTLLDLDQ 59
DB 32 EASGIGPEHPEVDEIRP-MGPVCPFCQCHLRVVCSDGLDKVPDLPPDTLLDLDQ 90
QY 60 NKKITEIKDGPFKNLKNIHALILVNNKISKYSPGAFPLVLYLERLYLSKNOLKEIPKMP 119
DB 91 NKKITEIKDGPFKNLKNIHALILVNNKISKYSPGAFPLVLYLERLYLSKNOLKEIPKMP 150
QY 120 KTLQELRAHEHETKVRKVTENGKLNQMVIELGTNPLKSSGIGENAFQGMKLSYIRAD 179
DB 151 KTLQELRAHEHETKVRKVTENGKLNQMVIELGTNPLKSSGIGENAFQGMKLSYIRAD 210
QY 180 TWTISIPQGLPPLSTELHLDGKLSRVDAASIKGLNNAKLGLSFNSISAVDNGSLANTP 239
DB 211 TWTISIPQGLPPLSTELHLDGKLSRVDAASIKGLNNAKLGLSFNSISAVDNGSLANTP 270
QY 240 HREHLHDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKASYSVGL 299
DB 271 HREHLHDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKASYSVGL 330
QY 300 FANPQVWEIOPSTRCYVVSATQLGNKY 329
DB 331 FANPQVWEIOPSTRCYVVSATQLGNKY 360

RESULT 3

147020
decorin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
C/Accession: 147020
R/Zhan, Q.; Burrows, R.; Cintonro, C.
Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995
A>Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.
A/Reference number: 147020; MUID:9512319; PMID:7822148
A/Accession: 147020
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-360 <ZNA>
A/Cross-references: GB:S76S84; NID:g913374; PIDN:AAB33083.1; PID:g913375
C/Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
F/49-73/Domain: proteoglycan amino-terminal homology <PAH>
F/83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F/107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR>
F/309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 91.3% Score 1564.5; DB 2; Length 360;
Best Local Similarity 90.6%; Pred. No. 3.7e-107;
Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 2;

QY 2 EASGIGBE -VPDDRDPPEPSLGVCPCPRQCQLRVVOCSDGLDKVPKDLPPDTLLDQ 59
 ||||| : |
DJ 32 EASGIGPERAPERELPDLD-MGVPCPRQCQHARVVQCSDDLGRKPVDLPDDTLLDQ 90
 ||||| : |
QY 60 NNKTTEIKDGDFKNLKNIHALILVNKKISKVSFGAFPLVLRLYLTKNLKEIPEKMP 119
 |||||||
DJ 91 NNKTTEIKDGDFKNLKNIHALILVNKKISKISPGAFPLVLRLYLTKNLKEIPEKMP 150
 |||||||
QY 120 KTIQELRAHEMEITKVRRVTENGINQMIVIELGNPLKSSEIENGAFCGMCKKSYIRAD 179
 |||||:
DJ 151 KSDELRAHEMEITKRKSVSPSGNMQMVIEIGNPLKSSGIENGAFGMCKKSYIRAD 210
 |||||:
QY 180 TNITSIPGGLEPSSLTELHLDGNKISRVDAASTKLGNLNAKIGLSFNSTSAVNGSLANTP 239
 |||||:
DJ 211 TNNITTPGGLEPSSLTELHLDGNKITKIDASSIKGLNLANAKIGLSFNDSIAVNGSLANAP 270
 |||||:
QY 240 HLRELAHDNNKLTRVPGGLAEHKYIQVVYLHNHNNTSVWSSSKDFCPGHNTKKAASYGSVL 299
 |||||:
DJ 271 HLRFLAHDNNKLIRVPGGLADHKYIQVVYLHNHNNTSVVGANDPCPGVNTTKKASYSVDSL 330
 |||||:
QY 300 FSNPVQYWEIFQPSTRFCRYVASAIOLGNKY 329
 |||||:
DJ 331 FSNPVQYWEIFQPSTRFCRYMRSALIOAGNYK 360
 |||||:

RESULT 4

S24317
decorin precursor - chicken
N/Alternate names: corneal chondroitin/dermatan sulfate proteoglycan
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 20-Aug-1999
C/Accession: S24317; S58474; S22197
R/Lil, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.
Arch. Biochem. Biophys. 296, 190-197, 1992
A>Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals
A/Reference number: S24317; MUID:92296755; PMID:1605630
A/Accession: S24317
A/Molecule type: mRNA
A/Residues: 1-357 <LIN>
A/Cross-references: EMBL:X63797; NID:g62887; PIDN:CBA45318.1; PID:g62888

A:Accession: SS8474
A:Molecule type: protein
A:Residues: 31-33, 'X', 35-39, 'X', 41-48, 'X', 50-51 <LIA>
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycans
C:Keywords: collagen binding; extracellular matrix; glycoprotein
F:1-16/Domain: signal sequence #status predicted <Sig>
F:17-30/Domain: propeptide #status predicted <Pro>
F:31-35/Product: decorin #status experimental <MAT>
F:46-70/Domain: leucine-rich amino-terminal homology <PAH>
F:80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:244-267/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:268-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <PCH>
F:306-357/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 82.6%; Score 1415; DB 2; Length 357;
Best Local Similarity 80.2%; Pred. No. 3.3e-96;
Matches 264; Conservative 28; Mismatches 37; Indels 0; Gaps 0;

QY 1 VEASGIGPEVPDDRDPFBSLGFVCPFCOCHLRVVCSDLGDKVPKDLPPDTLLDLQN 60
DB 29 IEDESSADMAPDPDDEVISGFGVCPFCOCHLRVVCSDLGELRPVDPDLPPDTLLDLQN 88
QY 61 NKRTIEIKGDFPNLKNLHALIIVNNKISVSPGAPFLPYKLEBYLSTKNDLKEPEKMPK 120
DB 89 NKRTIEIKGDFPNLKNLHALIIVNNKISKISPAAPFLKLEBYLSTKNDLKEPEKMPK 148
QY 121 TLOELRAHENETTKYRKVTFENGIANQMIYVELGTNPFKSSGIEGAPQGMKKLSTYRIADT 180
DB 149 SLOELRAHENETSKLRKAVFNGLNQIVYELGNPLKSSGIEGAPQGMKKLSTYRIADT 208
QY 181 NITSIPQGLPESLTSLHDGNTKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTPH 240
DB 209 NITSIPKGLPESLTSLHDGNTKISKIDAGLSGLTMLAKLGLSFNSISVENGSLANVPH 268
QY 241 LRELHLDDNNKLTFRVYGGLAEHKTYQVYVLAHNNISVVGSSDFPCPGNNTKKASISGVSIF 300
DB 269 LRELHLDDNNKLTFRVYGGLAEHKTYQVYVLAHNNISVVGSSDFPCPGNNTKKASISGVSIF 328
QY 301 SNPVQYWEIOPSTPCVYVSATOLGNKY 329
DB 329 SNPVQYWEIOPSTPCVYVSATOLGNKY 357

RESULT 5
A55454
N:Alternat names: proteoglycan II
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 20-Aug-1999
C:Accession: A55454; S20812
R:Scholzen, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan, J.L.; Buchberg, A.M.; Sliemers, L.P.
A:Title: The murine decorin. Complete cDNA cloning, genomic organization, chromosomal location, and expression of the gene.
A:Reference number: A55454; PMID:95050610; PMID:7961765
A:Accession: A55454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <SCH>
A:Cross-references: GB:X53929; NID:953668; PIDN:CAA37876.1; PID:953669
R:Naitoh, Y.; Suzuki, S.
A:Submitted to the EMBL Data Library, July 1990
A:Description: Nucleotide sequences of cDNAs encoding mouse FGI and FGI1.
A:Reference number: S20811
A:Accession: S20812
A:Status: preliminary
A:Molecule type: mRNA

F/161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/42,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F/271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.5%; Score 985.5; DB 2; Length 369;
Best Local Similarity 57.6%; Pred. No. 1e-64;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEPLSGVPCFPCQCHLRVQCSDDLGLDKVPKDLPTDTLLDQ 59
DB 40 EASGSDTTSQVDDLSVTPFSAFCPCFCHLRVQCSDDLGLDKVPKDLPTDTLLDQ 99

QY 60 NNKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSNQKELPEKMP 119
DB 100 NNDSIELRKDDPKGLOHLYALVNNKISKIHEKAFSPRLKQKLYISQNHVEIRPNP 159

QY 120 KTLQELRAHENEITKRYKTPNGINOMVIEIGTNPFKSSGIEBNGAFQGMKLSYRIAD 179
DB 160 SSLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGNGPLENSGEPGAFDGL-KLNTYLRIS 218

QY 180 TMTISIPQGLPSLTELHLDGNKISRVDASLKGNNLAKLGLSFNSISAVNGSLAMP 239
DB 219 AKLTGIPKDLPTLWELHLDHNNKIQALIELEDLIRYSKLRIGLGHNOIMTENGSLFIP 278

QY 240 HLREHLDDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVSSDFPCPGHNTKASYSVGL 299
DB 279 TLREHLDDNNKLSRPVAGLPDLKLQVYLLHNNNITKVGINDPCPGFVKAYVNGISL 338

QY 300 FSNPVQYWEIOPSTRFCYVYRSLAIOGNK 329
DB 339 FNNPVYWEVQPATFRCTVDRLAIOGNK 368

RESULT 8
S20811
proteoglycan I - mouse
N/Alternate names: biglycan
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #ext_change 20-Aug-1999
C/Accession: S20811; A57645; I49534
R/Alston, Y.; Suzuki, S.
submitted to the EMBL Data Library, July 1990
A/Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGI1.
A/Reference number: S20811
A/Accession: S20811
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <NAI>
A/Cross-references: EMBL:X53928; NID:953666; PID:CAA37875.1; PID:953667
R/Wegrowski, Y.; Pillarsetti, J.; Danielson, K.G.; Suzuki, S.; Iozzo, R.V.
Genomics 30, 8-17, 1995
A/Title: The murine biglycan: complete cDNA cloning, genomic organization, promoter function
A/Reference number: A57645; MID:9612925; PMID:8595907
A/Accession: A57645
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-67, 'W', 69-369 <WEG>
A/Cross-references: GB:L02076; NID:9348961; PID:AAA64360.1; PID:9348962
A/Note: authors translated the codon TGG for residue 58 as Cys
R/Kau, W.; Just, W.; Vetter, U.; Vogel, W.
Mamm. Genome 5, 395-396, 1994
A/Title: A dinucleotide repeat in the mouse biglycan gene (EST) on the X chromosome.
A/Reference number: I49534; MID:94319093; PMID:8043360
A/Accession: I49534
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-67, 'W', 69-369 <RES>
A/Cross-references: GB:L02076; NID:9348961; PID:AAA64360.1; PID:9348962
C/Genetics:
A/Gene: Bgn
C/Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C/Keywords: chondroitin sulfate, proteoglycan, dermatan sulfate, extracellular matrix;
F/58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F/317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>

Query Match 57.5%; Score 984.5; DB 2; Length 369;
Best Local Similarity 57.6%; Pred. No. 1.2e-64;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEPLSGVPCFPCQCHLRVQCSDDLGLDKVPKDLPTDTLLDQ 59
DB 40 EASGSDTTSQVDDLSVTPFSAFCPCFCHLRVQCSDDLGLDKVPKDLPTDTLLDQ 99

QY 60 NNKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSNQKELPEKMP 119
DB 100 NNDSIELRKDDPKGLOHLYALVNNKISKIHEKAFSPRLKQKLYISQNHVEIRPNP 159

QY 120 KTLQELRAHENEITKRYKTPNGINOMVIEIGTNPFKSSGIEBNGAFQGMKLSYRIAD 179
DB 160 SSLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGNGPLENSGEPGAFDGL-KLNTYLRIS 218

QY 180 TMTISIPQGLPSLTELHLDGNKISRVDASLKGNNLAKLGLSFNSISAVNGSLAMP 239
DB 219 AKLTGIPKDLPTLWELHLDHNNKIQALIELEDLIRYSKLRIGLGHNOIMTENGSLFIP 278

QY 240 HLREHLDDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVSSDFPCPGHNTKASYSVGL 299
DB 279 TLREHLDDNNKLSRPVAGLPDLKLQVYLLHNNNITKVGINDPCPGFVKAYVNGISL 338

QY 300 FSNPVQYWEIOPSTRFCYVYRSLAIOGNK 329
DB 339 FNNPVYWEVQPATFRCTVDRLAIOGNK 368

RESULT 9
S32559
biglycan precursor - bovine
N/Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin core p
C/Species: Bos primigenius taurus (cattle)
C/Date: 03-May-1994 #sequence revision 20-Feb-1995 #ext_change 07-May-1999
C/Accession: S32559; S34229; A33701; A31430; PT0078; S55673; A33137
R/Torok, M.A.; Evans, S.A.S.; Marcum, J.A.
Biochim. Biophys. Acta 1173, 81-84, 1993
A/Title: cDNA sequence for bovine biglycan (PGI) protein core.
A/Reference number: S32559; MID:93250052; PMID:8485158
A/Accession: S32559
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <TOR>
A/Cross-references: EMBL:L07953; NID:9162746
A/Experimental source: aortic smooth muscle
R/Marcum, J.A.; Torok, M.; Evans, S.
submitted to the EMBL Data Library, December 1992
A/Reference number: S34229
A/Accession: S34229
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-250, 'V', 252-369 <MAR>
A/Cross-references: EMBL:L07953
R/Name, P.U.; Choi, H.U.; Rosenberg, L.C.
J. Biol. Chem. 264, 8653-8661, 1989

A>Title: The primary structure of the core protein of the small, leucine-rich proteoglycan
A.Reference number: A33701; MUID:89255324; PMID:2656687

A.Accession: A33701

A.Molecule type: Protein

A.Residues: 38-187,'E','I',189-367,'Y' <NE>

A.Experimental source: Cartilage

R.Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.

J.Biol. Chem. 264, 2876-2884, 1989

A.Title: Characterization of the dermatan sulfate proteoglycans,^a DS-PGI and DS-PGII, from A.Reference number: A31430; MUID:89123388; PMID:2914936

A.Accession: A31430

A.Molecule type: Protein

A.Residues: 38-41,'X','43-47','X','49-63 <CHO>

A.Note: sequences from skin and cartilage were identical

R.Marum J.A.; Thompson, W.A.

Biochem. Biophys. Res. Commun. 175, 706-712, 1991

A>Title: The amino-terminal region of a proteochondroitin core protein, secreted by aortic om human bone.

A.Reference number: PT0077; MUID:91207372; PMID:2016513

A.Accession: PT0078

A.Molecule type: Protein

A.Residues: 17-24,'F','26-30 <MA>

A.Experimental source: aortic smooth muscle

F.Scott, P.G.; Nakano, T.; Dodd, C.M.

Biochim. Biophys. Acta 1244, 121-128, 1995

A>Title: Small proteoglycans from different regions of the fibrocartilaginous temporomaxilla Reference number: S55673; MUID:95284073; PMID:776647

A.Accession: S55673

A.Molecule type: Protein

A.Residues: 38-41,'X','43-47','X','49-53 <SCO>

C.Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan C Keywords: cartilage; chondroitin sulfate proteoglycan; dermatan sulfate; extracellular F.I-16/Domain: signal sequence #status predicted <SIG>

F.I-17/Domain: amino-terminal propeptide #status predicted <PRO>

F.I-369/Product: biglycan #status predicted <MA>

F.I-58-82/Domain: proteoglycan amino-terminal homology <PAH>

F.I-92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F.I-116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F.I-140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F.I-161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F.I-185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F.I-210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F.I-231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F.I-255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F.I-279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F.I-302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology atypical <LAR>

F.I-317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>

F.I-42,48/Binding site: dermatan sulfate (Ser) (covalent) #status experimental

P.I-181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted

P.I-271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Db 279 TLRRLHLDDNNKLSRVRAGLPEDLKLVVYLTHTNNITRVGVNDPFCVPGVGRATYYNGISL 338

QY 300 FSNPVQYWEIQSTFRCVYRSALIQGNKY 329

Db 339 FNNPVPYWEVQPAFRCTVDRLAIQFGNKY 368

RESULT 10

BGNUN
biglycan precursor - human
N.Alternate names: cartilage proteoglycan I; dermatan sulfate proteoglycan I (DS-PGI)
C.Species: Homo sapiens (man)
C.Date: 21-Apr-1992 #sequence revision 26-May-1995 #text change 28-Jan-2000
C.Accession: A40757; 138706; A32458; S14349; S05639; A28457
R.Fisher, L.W.; Heegaard, A.W.; Vetter, U.; Vogel, W.; Just, W.; Termine, J.D.; Young
J. Biol. Chem. 266, 14371-14377, 1991
A.Title: Human biglycan gene. Putative promoter, intron-exon junctions, and chromosomal
A.Reference number: A40757; MUID:91317791; PMID:1660845
A.Accession: A40757
A.Molecule type: DNA
A.Residues: 1-368 <FIS1>
A.Cross-references: GB:M65151; NID:q179428; GB:M65152; NID:q179429; GB:M65153; NID:q1
A.Note: the translated sequence in GenBank entry HUMBGN3, release 113.0, (PIDN:AAA52222;
d not the DNA) and 26 residues inserted after residue 80 (apparently from a misread s)
R.Just, W.; Rau, W.; Miller, R.; Geertkens, C.; Vogel, W.
Hum. Mol. Genet. 3, 2268, 1994
A.Title: Dinucleotide repeat polymorphism at the human biglycan (BGN) locus.
A.Reference number: 138706; MUID:95187185; PMID:7881444
A.Accession: 138706
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 361-368 <UTS>
A.Cross-references: EMBL:U11686; NID:g607862; PIDN:AAC50117.1; PID:9619663
R.Fisher, L.W.; Termine, J.D.; Young, M.F.
J. Biol. Chem. 264, 4571-4576, 1989
A.Title: Deduced protein sequence of bone small proteoglycan I (Biglycan) shows homology
A.Reference number: A32458; MUID:89174714; PMID:2647739
A.Accession: A32458
A.Molecule type: mRNA
A.Residues: 1-138, 'NV', 141-162, 'DV', 165-368 <FIS2>
A.Cross-references: GB:J04599; NID:q18439
A.Note: parts of this sequence, including the amino end of the mature protein, were d
R.Stoecker, G.; Meyer, H.E.; Wagener, C.; Grelling, H.
Biochem. J. 274, 415-420, 1991
A.Title: Purification and N-terminal amino acid sequence of a chondroitin sulphate/de
A.Reference number: S14349; MUID:91174749; PMID:1648758
A.Accession: S14349
A.Molecule type: protein
A.Residues: 38-57 <STO>
A.Experimental source: aorta
R.Roughley, P.J.; White, R.J.
Biochem. J. 262, 823-827, 1989
A.Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties
A.Reference number: S05639; MUID:90073579; PMID:2590169
A.Accession: S05639
A.Molecule type: protein
A.Residues: 38-41, 'X', 43-46, 'X', 48-57 <ROU>
R.Fisher, L.W.; Hawkins, G.R.; Thross, N.; Termine, J.D.
J. Biol. Chem. 262, 9702-9708, 1987
A.Title: Purification and partial characterization of small proteoglycans I and II, bc
A.Reference number: A28457; MUID:87250639; PMID:3597437
A.Accession: A28457
A.Molecule type: protein
A.Residues: 38-41, 'X', 43-62, 'X', 64-66 <FIS3>
A.Experimental source: bone
C.Genetics:
A.Gene: GDB:BGH
A.Cross-references: GDB:119727; OMIM:301870
A.Map position: Xq28-Xq28
A.Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
C.Superfamily: decorin, leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
C.Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; duplication; extracellu

R/1-16/Domain: signal sequence #status predicted <SIG>
R/1-17-37/Domain: propeptide #status predicted <PRO>
F/38-368/Product: biglycan #status predicted <MPT>
F/57-61/Domain: proteoglycan amino-terminal homology <PAH>
F/91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F/115-136/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F/139-159/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/184-207/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/209-229/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/230-253/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/254-277/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/301-315/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/316-366/Domain: proteoglycan carboxy-terminal homology <PCX>
F/442-47/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
F/180-199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F/270-311/Binding site: carboxymate (Asn) (covalent) #status predicted

Query Match	57.2%	Score 979;	DB 1;	Length 368;
Best Local Similarity	57.4%	Pred. No.3.1e-64;		
Matches 189;	Conservative 50;	Mismatches 88;	Indels 2;	Gaps 2;

[illegible]

RESULT 11

139068
 protein- arginine-rich and leucine-rich repeat protein PRELP precursor - human
 C.Species: Homo sapiens (man)
 C.Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999
 C.Accession: I39068
 R.Bengtsson, E., Neame, P.J., Heinegard, D., Sommarin, Y.
 U.Biol. Chem. 270, 25639-25644, 1995
 A.Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found in c
 A.Reference number: I39068; MUID:96029653; PMID:7592739
 A.Accession: I39068
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-382 <RCS>
 C.Cross-references: EMBL:U2089; NID:g886135; PIDD:AAC50230.1; PID:g886136
 C.Genetics:
 A.Gene: GDB:PRELP
 A.Cross-references: GDB:696218
 A.Map position: 1q32.1-1q32.1
 C.Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
 C.Keywords: tandem repeat

Query Match	22.5%	Score 385.5	DB 2	Length 382
Best Local Similarity	31.5%	Pred. NO. 1e-20		
Matches 91	Conservative	59	Mismatches 124	Indels 15
			Gaps	6

```

QY      2  EASGIGPEVPDRDDEPSLGLGVCPPRCQC---HLRVQCSDDGLDGVPPDLPTDTLLDL  58
Db      54  EPTDLPPLPPEG---PSGIFPDCPRECTCPDPFSALYCDSDNRKRVV-IPPRHHLYL  109

QY      59  QNNKTTTELKQGDPKYLKYLHALLLYNNKISKYSPGAFTPLVLYLELYLSKNQLKEAPEKM  118
Db      110  QNNFTPLPVESFQVATGIRWIMLNDLNRIRKIDORVLEKPGIVFLYMERKNQLEVPFSA  165

QY      119  PKTLOELBAHENEIKRVKRVTFENGDNOMIVIEGTNPFLKSGSGLENAQFQMKGLSYTIRA  178
Db      170  PRNLPEQLLSQNHISRIPEGVPSKLENNILLDLQNNRLSDGVFKPPTFFHGLKYLMLQNLIA  229

QY      179  DTNITSIFQGLPPSITELHLDGNKISRVDAAASKGLNNIATLGLSFGNSIAVDNG---SL  235
Db      230  HNIILKQMPRPVETAHOLYLDNSNKEITIPNGYEFKSPNIAFIRLANNKLT--DRGLPKNS  287

QY      236  ANTPHLRELHLDNNKLTVPGSLAHHKYIOVYLIHNNNSIYVGGSDPFC  284
Db      288  FNISNLVLHLSHNRISVPP--AINNRLEHLYNNNSIEKINGTQICP  333

```

RESULT 12

lumican precursor - chicken
M.Alternate names: corneal keratan sulfate proteoglycan
C.Species: Gallus gallus (chicken)
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 04-Sep-1998
A.Accession: A41748, B41748
R.Blochberger, T.C.; Vergnes, J.P.; Hempel, J.; Hassell, J.R.
J. Biol. Chem. 267, 347-352, 1992
A.Title: cDNA to chick lumican (corneal keratan sulfate proteoglycan) reveals homology
A.Reference number: A41748; MIMD:92112674; PMID:1370446
A.Accession: A41748
A.Molecule type: mRNA
A.Residues: 1-343 <BL1>
A.Cross-references: GB:M80584
A.Accession: B41748
A.Molecule type: protein
A.Residues: 55-76 <BL2>
C.Superfamily: fibromodulin, leucine-rich alpha-2-glycoprotein repeat homology
C.Keywords: glycoprotein; tandem repeat
F.1-18/Domains: signal sequence #status predicted <SIG>
F.19-343/Product: lumican #status predicted <MT>

Query Match	21.3%	Score 365.5;	DB 2,	Length 343;
Best Local Similarity	31.9%	Pred. No. 2.5e-19;		
Matches 108;	Conservative 58;	Mismatches 146;	Indels 27;	Gaps 11

```

4 SGI-----GPEVPDDRDFFESPJGP---VCPFRQCHL---RVQSCDLDGLBKVPKDLPP 51
||| ||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 14 SGIFCQYDYG--ADDYGYDP-FGPSTAVCAPECNCPLSYPTAMYCDNLKLTIP-IVPS 69

1. **THE STATE OF TEXAS, COUNTY OF DALLAS, ss. I, _____, Clerk of the County Court, do hereby certify that the within and foregoing is a true and correct copy of the original as the same appears from the records of the County Court of Dallas County, Texas.**

52 DYTLLDQNNKI TEIKOGDFKLNKLHALILVNNKI--SKVSPGAFPLVKLERLYLSKN 100

70 GIKYI YI PNMT EAT EENT EONT DI OWI TI DNHI ENSK TGPV ESKI KNI KKI HTNYN 1 2

10 9 8 7 6 5 4 3 2 1

110 QLKELPEKMPKTLQELRAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGM 160

[illegible]

Db 130 NLTEAVGRLPKTLDDLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDISI-SGAFFKGL 18

THE UNIVERSITY OF CHICAGO

170 KLSYIRADNTITSIPQGLPPSLTEHLHDGNKISRVDASLKGJLNLAKLGLSFSISA 22

Db 100 NSTI YI DI GENOI TKI BTGI BHSI I MI YEDNNOT SNT BDEVEOGEKTI OVI PI SHNKT T- 24

DB 189 NSULIWLDSFNQULIALPIGLPHSLMLLIFDNNQISNLPDEIFQGFALDQILKLSHNNKLI - 24

OV 230 VDN---GSLANTPHILREHLDNKCLTRVPGIAEHKYIOVYLIHNNNISVVGSSDFCPCG 28

[illegible]

Db 248 -DSGIPGNVFNITSLVELDLSFNQKSIPTVSENLENFYLQVNKINKFPLSSFCKVV 3C

QY 287 HNTKKASYSGVSLFSNPQYWEIQPSTFRVCYVRSAIL 325

[illegible]

DB 304 GFLIYSKJTHLRDGNNTKADLPQEMXNCLRVAADISL 342

RESULT 13

A46743

luminan precursor - bovine

N/Alternate names: 37k keratan sulfate-linked protein; corneal keratan sulfate proteoglycan

C/Species: Bos primigenius taurus (cattle)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999

C/Accession: A46743; A53379

R/Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 268, 11874-11880, 1993

A/Title: Sequence and structural implications of a bovine corneal keratan sulfate proteoglycan

A/Reference number: A46743; MUID:93280153; PMID:8099356

A/Accession: A46743

A/Molecule type: mRNA

A/Residues: 1-342 <FNU>

A/Cross-references: GB:L11063; NID:9163266; PIDN:AAA30608.1; PID:9163267

A/Experimental source: cornea

R/Funderburgh, J.L.; Conrad, G.W.

J. Biol. Chem. 265, 8297-8303, 1990

A/Title: Isoforms of corneal keratan sulfate proteoglycan.

A/Reference number: A53379; MUID:90243714; PMID:2135877

A/Accession: A53379

A/Molecule type: protein

A/Residues: 19-36 <F02>

A/Experimental source: cornea

C/Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

C/Keywords: glycoprotein; tandem repeat

F1-18/Domains: signal sequence #status predicted <SIG>

F19-342/Product: luminan #status predicted <MAT>

F192,131,164,256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.8%; Score 356.5; DB 2; Length 342;

Best Local Similarity 31.7%; Pred. No. 1.1e-18;

Matches 107; Conservative 57; Mismatches 143; Indels 31; Gaps 12;

QY 3 ASGIGPEVDDRDPEPSL---GPVCPFRCC---HLRVCCSDGLDKVPEKDLPPDTTL 55

DB 16 ASSTPYDYEEYDFQALYGRSPRCAPCECPESYPSAMCDELKLSVPM-VPPGKTY 74

QY 56 LDQNNKTEIKDGFQKLNILVNNKI--SKVSPGAFPLVLERLYLSKNOQKE 113

DB 75 LYLNNQIDHIDDKAFENVTDLOWLIDHNLENSKIKGVFSKQKQKLIHNNVNLTE 134

QY 114 LPEKPKTLOELRAHNEITVRYKTFNGLNQMIYIEGTPIKSSGIEGNAFOGMKLS 173

DB 135 SVGPPLKSLVDLQLTNNKISKLG--SPDGLVNLFTFHLQHQLKEDAV-SALNGLKSLR 191

QY 174 YIRIADTNTSIPOGLPSTLHLDGKISRVDASLKGKLNIAKLGISFNSI--SAVD 231

DB 192 YLDSFNMOTKLPSGLPVSLTLTYDNNKISINIPDEYKRSALQYLRISHNELADSGVP 251

QY 232 NGSLANTPHLEHLIDNNKLTFRVPGLAHEKRYIQVYLAHNNNISVSSGSDPC--PGHN 288

DB 252 GNSF-NVSSLELDELSTYKLSIP---TVNENLENYYLEVNELEKFDVSKILIGP--- 304

QY 289 TKKASYSQVS---LFSNPVQWEIOPSTFRCVYRSAL 323

DB 305 ---LSYSKIKHLRDGNHITQTSPLPDWYECGLRVANEI 339

RESULT 14

S52284

luminan, secretory interstitial proteoglycan precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999

C/Accession: S52284

R/Krull, N.B.

submitted to the EMBL Data Library, January 1995

A/Reference number: S52284

A/Accession: S52284

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-338 <KRU>

A/Cross-references: EMBL:X84039; NID:9643023; PIDN:CAA58858.1; PID:9643024

C/Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

Query Match 20.3%; Score 347.5; DB 2; Length 338;

Best Local Similarity 31.5%; Pred. No. 5.1e-18;

Matches 100; Conservative 56; Mismatches 134; Indels 27; Gaps 11;

QY 20 LGPVCPRCC---HLRVCCSDGLDKVPEKDLPPDTTLDLQNNKTEIKDGFQKLN 76

DB 33 LSPVCAPECNCPHSYPTAMCDDDLKLSVPM-VPPGKTYLYLRNNQIDHIDDKAFENVTD 91

QY 77 LHALILVNNKI--SKVSPGAFPLVLERLYLSKNOQKEPEKPKTLOELRAHNEITK 134

DB 92 LQWILIDHNLENSKIKGVFSKQKQKLIHNNVNLTEYSGPLKSLQDQLNNKISK 151

QY 135 VRKTFNGLNQMIYIEGTPIKSSGIEGNAFOGMKLSYIRIADTNTSIPOGLPSTLT 194

DB 152 LG--SPDGLVNLFTFHLQHQLKEAV-SASIKLKSLEYLDLSFNMQSKLPAGLPSTLT 208

QY 195 ELHIDGKISRVDASLKGKLNIAKLGISFNSI--SAVDNGSLANTPHLEHLIDNNKLT 252

DB 209 TLYIDNNKITNIPDEYFNRFQGLQYLRISHNELADSGVPGNSF-NISLLELDLSYNDLK 267

QY 253 RVPGLAEHKYIQVYLAHNNNISVSSGSDPC---PGHNTKASYSQVS---LFSNPVQY 306

DB 268 SIP---TVNENLENYYLEVNELEKFDVSKILIGP-----LSYSKIKHLRDGNPLTO 318

QY 307 WEIQSTFRCVYRSAL 323

DB 319 SSLPDDWYECGLRVANEI 335

RESULT 15

slit-1 protein homolog - rat

N/Alternate names: MEQF4 protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002

C/Accession: T42218

R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A/Reference number: Z14126; MUID:98360089; PMID:9633030

A/Accession: T42218

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1531 <NAK>

A/Cross-references: EMBL:AB011530; NID:93449289; PIDN:BA32460.1; PID:93449290

A/Experimental source: strain Sprague-Dawley; brain

C/Genetics:

A/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 19.1%; Score 327.5; DB 2; Length 1531;

Best Local Similarity 24.9%; Pred. No. 1.2e-15;

Matches 96; Conservative 65; Mismatches 122; Indels 103; Gaps 9;

QY 10 VPDDRDF---EPLAGVCPFCQCCHLRVQCCDGLDKVPEKDLPPDTTLDLQNNKITE 65

DB 495 IPTGEDIHNSSECTSDVACPHKCRCEASVYECGGLSKIPERIPSTTELRANNNEIS1 554

QY 66 IK-DGDFKKNILHALILVNNKISKVSFGAFPLVLERLYLSKNOQKEPEKPKTLOE 124

DB 555 LKATGELPKKLSHKKINILSNKKVSEIDGTFEGATGSEIHLTPANQLESYRSGWFRIGD 614

QY 125 LRA---HENELTYKRYKTFNGLNQMIYIEGTPIKSSGIEGNAFOGMKLS----- 173

DB 615 LRTLMNNRISCIHNSDFTGLRNVRLLSLYDNHITT--LSPGAFDTQLALSTLNLAMP 672

QY 174 ----- 173

DB 673 FNCNCQLAWLGRKKKIVTGNPRQGNPDLQIPLQDVAFPDFRCEBGBGVGCLRP 732

QY 174 -----YIRADTNTISIPQGLPSLTETLHLDGNKISRVDAAASIKGLNNTLAKGL 222
Db 733 QCPQACADIVYRCNKKGLALPKGIPKNNTELYLDGQFTLV-PGQSTFKYQLQVLD 791
QY 223 SFNSISAVDNGSLANTPHILREHLDDNNKLTTRVP---GGLAHKKYIQVYLLHNNNISVVG 278
Db 792 SNNKISSLSNSSFMTNMSQLTTLTSLYNALQICIPPLAQFL---RSIRLSTLHGNDVSTLQ 848
QY 279 SSDPCPRGHNTKKASYSYGSVLSFNPV 304
Db 849 EGIF-----ADVTLSHLAIGANPL 868

RESULT 16

T13953
MEGF5 protein - rat
N:Alternate names: slit protein homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C:Accession: T13953
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; PMID:98360089; PMID:9693030
A:Accession: T13953
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-153 <NAK>
A:Cross-references: EMBL:AB011531; NID:G3449291; PIDN:BAA32461.1; PID:G3449292
C:Genetics:
A:Gene: MEGF5
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
Query Match 19.1%; Score 327; DB 2; Length 1523;
Best Local Similarity 24.9%; Pred. No. 1.3e-15;
Matches 99; Conservative 53; Mismatches 124; Indels 122; Gaps 7;
QY 21 GP---VCPRCQCHLVVQCSDLGDKVPKDLPPDTLLDQNNKLTETKDGPKYKLN 77
Db 28 GPPAAACPTKCTCSAASVDCGGLGRVAPRGIPRNARRLDLDRNNTRITKMPFTGLKN 87
QY 78 HALLVNNKISKVSPGAFPLVLEKRLYLSKNQKELPEKM---PRTYQELRAHNEIT 133
Db 88 RVHLIEDNQSVIERGAFQDLKQLERLRNKNLQVLPPELLPOSTRK-LTRLDLSNQIQ 146
QY 134 KVRKVTENGINQMIETELGTPNPKSSGIEGAFQGMKKLSYIRADNTI----- 182
Db 147 GIPKAFRGVYGVKNQLDNNHI--SCIEDGAFRALDLEILTLNNNNISRIILVTSFNM 204
QY 183 ----- 182
Db 205 PKIRTLRLSHNLVCDCHLAWLSDWLRQRTTIGQFTLCMAVPHLRGFSVADQKKEVCP 264
QY 183 -----TSIPQGLPPLSTELHLDGNKISRVD 208
Db 265 GPHSEAPACNANSLSCPSACSNIVYDCGKGLTEIPALPEGIVAIRLEQNSISIPA 324
QY 209 ASIKGLNNTLAKGLSFNSISAVDNGSLANTPHILREHLDDNNKLTTRVGLAEHKY-IQVV 267
Db 325 GAFTQYKQLKRIDISKQISDIAADAFQGLKSLTSLVYGNKLTETPKGFGDGLVSLQL 384
QY 268 YLENNNISVVGSSDFCPGHNTKKASYSYGSVLSFNPV 305
Db 385 LTNANKINCLRVTF-----QDLQNLNLTSLYDNKIQ 416

RESULT 17

S55275
fibromodulin precursor - human
N:Alternate names: 59K collagen-binding matrix protein
C:Species: Homo sapiens (man)
C:Date: 23-Aug-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
C:Accession: S55275; S35710; S32752; S41925

R:Hildebrand, A.; Romaris, M.; Rasmussen, L.M.; Heinegard, D.; Twardzik, D.R.
Biochem. J. 302, 527-534, 1994
A:Title: Interaction of the small interstitial proteoglycans biglycan, decorin and fib
A:Reference number: S55275; PMID:94379985; PMID:8093006
A:Accession: S55275
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-376 <H12>
A:Cross-references: EMBL:X75546; NID:G453156; PIDN:CAA53233.1; PID:G453157
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
R:Antonsson, P.; Heinegard, D.; Oldberg, A.
Biochim. Biophys. Acta 1174, 204-206, 1993
A:Title: Structure and deduced amino acid sequence of the human fibromodulin gene.
A:Reference number: S35710; PMID:93363641; PMID:8357838
A:Accession: S35710
A:Molecule type: DNA
A:Residues: 1-3, 'T', '5-86, 'P', '88-209, 'N', '211-225, 'Y', '227-343, 'Q', '345-354, 'W', '356-362, 'I
A:Cross-references: EMBL:X72913; NID:G297090; PIDN:CAA51418.1; PID:G297091
C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the a
C:Genetics:
A:Gene: GDB:PMOD
A:Cross-references: GDB:228979; OMIM:600245
A:Map position: 1q32.1-1q32.1
A:Insertions: 326/2
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-376/Product: fibromodulin #status predicted <MAT>
F:8,39,42,45,47,50,53,55,63,65/Binding site: sulfate (tyr) (covalent) #status predict
F:127,166,201,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 326.5; DB 2; Length 376;
Best Local Similarity 27.9%; Pred. No. 2.1e-16;
Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVPDDRDPEPSLGVCPFCOC---HLRVQCSDLGDKVPKDLPPDTLLDQNNKLT 64
Db 68 PSEPPDRD-----CPQECDCPPNFFLWAMCDNRNKLKLP-FVPSRMKVVYFQNNQT 118
QY 65 EIKDQDFQKULHALLVNNKIS--KSPGAFPLVLEKRLYLSKNQKELPEKPKLT 122
Db 119 SIOGVFDNATGTLWALHGNQITSDKVGKRYFSKLRHLERLYLDNNLTRMGPPLRS 178
QY 123 QELRAHNEITVYKRTFNGMIVIELGTPNPKSSGIEGAFQGMKKLSYIRADNTI 182
Db 179 RELHLDNNOISRVPNNALGLENTLALYLOHBEIQVG--SSMRGLRSLILDLDSYNH 235
QY 183 TSIPQGLPPLSTELHLDGNKISRVDAAASIKGLNNTLAKGLSFNSISAVDNGSLANT---P 239
Db 236 RKVPDGLPSALDELVEHNNVTVPSYFRGAPKLLYVRLSHNSLT--NNGLASNTFNS 293
QY 240 HREHLDDNNKLTTRVGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKASYSVSL 299
Db 294 SLLELDLSYNQLOKTP---PVNTLENLYLQGRINEFSISRCTVADVNVFSLQVRL 350
QY 300 FSNPVOYMEIQPSTFRQVYVSAIQ 325
Db 351 DGEIRSAMPADAPLCRLASLTET 376

RESULT 18

B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C:Accession: B36665
R:Rothenberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Arcavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A:Title: Slit: an extracellular protein necessary for development of midline glia and
A:Reference number: B36665; PMID:9109965; PMID:2176636
A:Accession: B36665
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-1469 <ROT>
A:Cross-references: GB:X53959
C:Genetics:
A:Gene: FlyBase:sl1
A:Cross-references: FlyBase:FBgn0003425
C:Superfamily: fruit fly salt protein; EGF homology; leucine-rich alpha-2-glycoprotein
F:66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F:323-346/Domain: proteoglycan amino-terminal homology <PAH2>
F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F:512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F:708-733/Domain: proteoglycan amino-terminal homology <PAH3>
F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:1028-1061/Domain: EGF homology <EGF1>
F:1068-1099/Domain: EGF homology <EGF2>
F:1115-1148/Domain: EGF homology <EGF1>
Query Match 18.9%; Score 323; DB 2; Length 1469;
Best Local Similarity 25.3%; Pred. No. 2,4e-15;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
Db 2 EASGIGPEVDDDRFSPSLGVPVCPFCQCHLRVQSGDLGDKVPKDLPPDTLLDLONN 61
277 KCSGLTEHAPMECGAENS-----CPHRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
Db 62 KITTEIKDGPKNLKNLHALLIVNNKISKVSFGAFTPLVLERLYLSKNQKELPERKPKT 121
333 FITELPKPSFSSFRRLRRIDLSNNNISRIADHLSGLKQTLTVLVGNKKIDLPSSGVFKG 392
Qy 122 LOELR---AHENETTKRKTYFNGLNQMIYIELGTNPDKSSGIENGAFOGKKLSTYRIA 178
393 LGSRLRLILNANETISCTIRKDAFRDLHSLSLSYDNNIQS--LANGTFAMKSMKTVHLA 450
Qy 179 -----DTN----- 181
Db 451 KNPIPCDNLRLWLDYLRHKNPIETSGARCESPKRMHRRRIEELREKFKCSWGELRMKLS 510
Qy 182 -----ITSIPQGLPSELTEHLDGKNKISRVDASLKG-L 214
Db 511 GECRMDSDCPAMGCHGCTVYDCTGRRLKEIPRODILPHTTELLANDNLGHSIGLGRLL 570
Qy 215 NNLAKEGLSPRSISIAVNGSLANTPHRLREHLDNNKLTTRVPGG--LAEHYTIQVYVLIANN 272
Db 571 PHLVKELKRNQQLGIEPNAFEGASHIQEQLQGENKIKESINRKFGLHQ-LKTLNLIYDN 629
Qy 273 NISVAGSSDFCPGPHNTKKASYSQVSLFSPN 303
Db 630 QIGCV-----MPSFEHLNLSITSLNLSNP 654

R:Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A:Title: salt: an extracellular protein necessary for development of midline glia and
A:Reference number: A36665; PMID:91099665; PMID:2176636
A:Accession: A36665
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1480 <ROT>
A:Cross-references: GB:X53959; NID:98614; PID:CA937910.1; PID:98615
R:Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A:Title: salt: An EGF-homologous locus of D. melanogaster involved in the development
A:Reference number: A31640; PMID:8907553; PMID:3144436
A:Accession: A31640
A:Molecule type: DNA
A:Residues: 861-1182, 'G', '1185-1404', 'GT', '1463-1464', 'YHA' <RO2>
A:Cross-references: GB:W23543; NID:9340939; PID:9514357
C:Genetics:
A:Gene: FlyBase:sl1
A:Cross-references: FlyBase:FBgn0003425
A:Interons: 1351/3
C:Superfamily: fruit fly salt protein; EGF homology; leucine-rich alpha-2-glycoprotein
C:Keywords: alternative splicing; growth factor
F:66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F:512-537/Domain: proteoglycan amino-terminal homology <PAH2>
F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F:708-733/Domain: proteoglycan amino-terminal homology <PAH3>
F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:1028-1061/Domain: EGF homology <EGF1>
F:1068-1099/Domain: EGF homology <EGF2>
F:1115-1148/Domain: EGF homology <EGF1>
Query Match 18.9%; Score 323; DB 2; Length 1480;
Best Local Similarity 25.3%; Pred. No. 2,4e-15;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
Db 2 EASGIGPEVDDDRFSPSLGVPVCPFCQCHLRVQSGDLGDKVPKDLPPDTLLDLONN 61
277 KCSGLTEHAPMECGAENS-----CPHRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
Db 62 KITTEIKDGPKNLKNLHALLIVNNKISKVSFGAFTPLVLERLYLSKNQKELPERKPKT 121
333 FITELPKPSFSSFRRLRRIDLSNNNISRIADHLSGLKQTLTVLVGNKKIDLPSSGVFKG 392
Qy 122 LOELR---AHENETTKRKTYFNGLNQMIYIELGTNPDKSSGIENGAFOGKKLSTYRIA 178
Db 393 LGSRLRLILNANETISCTIRKDAFRDLHSLSLSYDNNIQS--LANGTFAMKSMKTVHLA 450
Qy 179 -----DTN----- 181
Db 451 KNPIPCDNLRLWLDYLRHKNPIETSGARCESPKRMHRRRIEELREKFKCSWGELRMKLS 510

```

QY 182 -----ITSIPQGLPSSLTLEHLHDGKISRVDASLKL-214
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 511 GECRMDSDCPMCHCCHCTTVDCTGRRLKEIPRIPLHTTELLANDELGLISDGLFGRK 570
QY 215 NNIAKLGLSPNSISAVDNGSLANTPHRLREHLDDNNLTLVPGG--LAEHKYIQVYLVNHN 272
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 571 PHLVKELKRNQUTGIEBPNAFEGASHIQELQGENIKKISNMCFGLMQ-LKTLNLVYN 629
QY 273 NISVVGSSDFCPPGHNTKKAISVGSVLSFNSP 303
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 630 QISCV-----MGSFEHLNLSLTSLNLASNP 654

RESULT 20
S05390
Fibromodulin precursor - bovine
N:Alternate names: 59k collagen-binding matrix protein
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 24-Sep-1999
C:Accession: S05390; S26942; S06040
R:Oldberg, A.; Antonsson, P.; Lindblom, K.; Heinegard, D.
EMBO J. 8, 2601-2604, 1989
A:Title: A collagen-binding 59-kd protein (fibromodulin) is structurally related to the
A:Reference number: S05390; PMID:9060020; PMID:2531085
A:Accession: S05390
A:Molecule type: mRNA
A:Residues: 1-375 <OLD>
A:Cross-references: GB:X16485; EMBL:X16305; NID:g353; PIDN:CA434503.1; PID:g354
A:Accession: S26942
A:Molecule type: protein
A:Residues: 90-105;190-199;274-281 <OLD>
R:Plaas, A.H.K.; Neame, P.O.; Nivens, C.M.; Reiss, L.
J. Biol. Chem. 265, 20634-20640, 1990
A:Title: Identification of the keratan sulfate attachment sites on bovine fibromodulin.
A:Reference number: A23663; PMID:91056119; PMID:2243109
A:Contents: annotation; keratan sulfate attachment
C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the aspa
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective ti
F:1-18/Domain: signal sequence <status predicted <Sig>
F:19-375/Product: fibromodulin #status experimental <MAT>
F:38-42,45,47,50,53,62,64/Binding site: sulfate (Tyr) (covalent) #status predicted
F:126,165,200,230/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 18.4%; Score 314.5; DB 2; Length 375;
Best Local Similarity 29.6%; Pred. No. 1.6e-15;
Matches 84; Conservative 55; Mismatches 120; Indels 25; Gaps 8;

QY 8 PEVPRDRDEPSPISGVPFCRCQ--HLRVQCSDLGLDKVPKDLPPDTLLDLONNKIT 64
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 PQPPEPRD-----CPQECDCPPNFPPTAMYCDNNRLKTLF-FVPSRMKYVVFQNNQIS 117
QY 65 EIKDGFKXKLNHALILVNNKIS--KVPGAFTPLVKLERLYLSKQKELPEKPKTL 122
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 SIQEGVFDAATGLMALHGNQITSPKVGKQVSKRLHRLTLDDNNLRLRISPSRSL 177
QY 123 QELRAHENEITKRVKVTNGLNQMIYIELGTNPKSSGIEGNGAFQGMKLSYIRADPTNI 182
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 RELHLDHNGISRPNNALGLENLTALYLHNEIQGVG--SSMKGLRSILLLDLSYNH 234
QY 183 TSTPQGLPSSLTLEHLHDGKISRVDASLKLNNLAKLGLSPNSISAVDNGSLANT--P 239
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 RKVPDELPSALTEQLYLEHNNVFSPDPSYFSGSKLLYYRLSHNSLT--NNGLASNTFNS 292
QY 240 HLRELHLDNNKLTRVPGGLAEHKYIQVYLVNHNNSISVGSDDC 283
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 SLLELDLSTNQLKIP--PVSTNLENTLYLQGRINEFSISFC 333

RESULT 21
T42626
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N:Alternate names: neurogenic extracellular slit protein

```

```

C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2002
C:Accession: T42626
R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.
Mech. Dev. 79, 57-72, 1998
A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs
A:Reference number: Z22177; PMID:99279228; PMID:10346621
A:Accession: T42626
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1025 <HOL>
A:Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD04345.1
C:Genetics:
A:Gene: Slit2
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein;

Query Match 18.3%; Score 314; DB 2; Length 1025;
Best Local Similarity 25.4%; Pred. No. 6.7e-15;
Matches 100; Conservative 59; Mismatches 122; Indels 112; Gaps 11;

QY 24 CPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLONNKITEIK-DGDFKLNKLNHALIL 82
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 CPKRCCEGTVDSCSNRLNKIPDHIPQYTAELRLNNEFTVLAAGIFKKLPQLRXINF 61
QY 83 VNNKISKVPPGAFPLVKLERLYLSKQKELPEKPKTLQELRA-----127
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 SNNKRTDIEGAFEGASGVNEILLTSNRLNVOHKMFKGLSLKTLMSNRISCVGND 121
QY 128 -----HENETIKRVKVTNGLNQMIYIELGTNP-----155
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 FIGLGSVRLSLYDNOITTVAGAPKXLSLSTNLNLANPNCNHLAMGELRRKRIY 181
QY 156 -----LKSSGIENGAFQ-----GKKKLS-----YIRADPTNI 182
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 TGNPRCQKPYFLKPIQVVALQDPFCDDGNDNDCSPISRCPECTCLDTYVRCNNKL 241
QY 183 TSTPQGLPSSLTLEHLHDGKISRVDASLKLNNLAKLGLSPNSISAVDNGSLANTPHLR 242
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 KVLPKPIPDVVELYLDGQFLTV-PKELSNYKHLTLIDLSNRRISTLSNOKFSNNQTLL 300
QY 243 ELHLDNNKLTRP-----GGLAHKYIQVYLVNHNNSISVGSDDFCPPGHNTKASVGS 298
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 TLILSNRLRCIPPRFDGL--KSLRLISLHGNDSIV-----PEGAPNDLSALSHLA 351
QY 299 LPSNPV-----QYWEIQPSTFRC 316
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 IGANPLYCDQNNQWLSDWKSEYKE--PGIANC 382

RESULT 22
S71876
Fibromodulin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S71876
R:Nurmankaya, M.V.; Birk, D.E.
Biochem. J. 317, 785-789, 1996
A:Title: Differential expression of fibromodulin mRNA associated with tendon fibril g
A:Reference number: S71876; PMID:96332470; PMID:8760363
A:Accession: S71876
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-380 <NUR>
A:Cross-references: EMBL:U34977; NID:g1098905; PIDN:AAC60016.1; PID:g1098906
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

Query Match 17.4%; Score 298.5; DB 2; Length 380;
Best Local Similarity 30.1%; Pred. No. 2.4e-14;
Matches 81; Conservative 50; Mismatches 119; Indels 19; Gaps 7;

QY 24 CPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGFKLNKLNHALIL 80
| : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 CPQECDCPPNFPPTAMYCDNNRLKTLF-FVPTRMKYVVFQNNQITAIQGAFDNATELNL 138

```


QY 81 ILVNNKIS--KVSPGAFPLVYKLERLYLSKNQKLEPEKMPKTYOELRAHNEITKYKV 138
 Db 139 ALHNNQISSEKQKRVFAKLNKRLYNNNNNTMPSPRLPSRLREHLSTYQKSKVPSN 198
 QY 139 TFGNLQMWIVLELGTNPDKSSGIEGAFQKMKLSYRIADTNITSTIQGPPSLTEHL 198
 Db 199 ALBGLNLTALYLSHNYIFEMG---ASLQKSLILADLSYNHLRKVPDGLPMLEOLYL 255
 QY 199 DGNKISRVDASLKLGNLNLAKLGLSPNSISAVDNGSLA---NTPHLREHLDDNNKLT 254
 Db 256 EYNTINMIPDDYFKVSPPLLYVRMSHSLT---NQLSTNPNSSSIIELDLSNRLQKI 312
 QY 255 PGGLAEKRYIOVYVTLHNNNISVVGSSDFC 283
 Db 313 P--RVSTNENLYIQGQINEFSISSFC 338

RESULT 23
 JE0176
 orphan G protein-coupled receptor precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
 C/Accession: JE0176
 R/McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q.
 Biochem. Biophys. Res. Commun. 247, 266-270, 1998
 A/Title: Identification and cloning of an orphan G protein-coupled receptor of the glyco
 A/Reference number: JE0176; MUID:98308104; PMID:9642114
 A/Accession: JE0176
 A/Molecule type: mRNA
 A/Residues: 1-907 <MCD>
 A/Cross-references: GB:AF062006; NID:93366801; PID:MAC28019.1; PID:93366802
 C/Comment: This protein is a receptor for a novel class of glycoprotein ligands.
 C/Genetics:
 A/Gene: HG38
 A/Map position: 12q22-23
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:562-583/Domain: transmembrane #status predicted <TM1>
 F:594-616/Domain: transmembrane #status predicted <TM2>
 F:639-660/Domain: transmembrane #status predicted <TM3>
 F:661-701/Domain: transmembrane #status predicted <TM4>
 F:725-744/Domain: transmembrane #status predicted <TM5>
 F:768-791/Domain: transmembrane #status predicted <TM6>
 F:803-824/Domain: transmembrane #status predicted <TM7>

Query Match 17.3%; Score 295.5; DB 2; Length 907;
 Best Local Similarity 30.3%; Pred. No. 1.3e-13;
 Matches 82; Conservative 50; Mismatches 124; Indels 15; Gaps 6;
 QY 24 CFFRCQCH----LRVQCSDLGDKVYKDLPPDTLLDQNNKITEIKDGFKNLNLH 78
 Db 34 CPHCHCEPDGRMLLRVDCSDLGSELPSNLSVFTSYLDSMNNISQGLPPLPSLAFLE 93
 QY 79 ALIIVNNKISKVSFGATPLVYKLERLYLSKNQKLEPEK---PKTQELRAHNEITKY 135
 Db 94 ELRLAGALTYIPKGAFTGYSLKVLMLQNNQLAHVTEALQMLRSQSLRLDANHISYV 153
 QY 136 RKYTFNGLQMWIVLELGTNPDKSSGIEGAFQKMKLSYRIADTNITSTIQG---GLPSP 192
 Db 154 PRSCFSLSHLRHMLDDNLTEIPVQ--AFRSLALQMTALINKLHHIPDYAFGLSS 211
 QY 193 LTELHLQNKISRVDASLKLGNLNLAKLGLSPNSISAVDNGSLANTPHLEHLDDNNKLT 252
 Db 212 LVVTLHNNRIHSLGKCCPDGLSHLETLDTANNYLNDEFP--AIRTLNLKELGPHSNIR 270
 QY 253 RVP--GGGLAEKRYIOVYVTLHNNNISVVGSSDF 282
 Db 271 SIPEKAFVGNPSLITTHFYDNPYQVGRSAF 301

RESULT 24
 A53860
 chondroadherin precursor - bovine

N/Alternate names: 38k leucine-rich protein
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
 C/Accession: A53860
 R/Name: P.U.; Sommarin, Y.; Boynton, R.E.; Heinegard, D.
 J. Biol. Chem. 269, 21547-21554, 1994
 A/Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated fro
 A/Reference number: A53860; MUID:94342341; PMID:8063792
 A/Accession: A53860
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-361 <NEA>
 A/Cross-references: GB:U08018; NID:9470671; PID:AAA21330.1; PID:9470672
 C/Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox
 C/Keywords: disulfide bond
 F:300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 17.1%; Score 293; DB 2; Length 361;
 Best Local Similarity 27.4%; Pred. No. 5.6e-14;
 Matches 92; Conservative 67; Mismatches 129; Indels 48; Gaps 11;
 QY 18 PSIGVCPFRQCH--LRVQCSDLGDKVYKDLPPDTLLDQNNKITEIKDGFKNL 75
 Db 20 PALA-ACPQNGCHSDLOHVI CDKVGLOKIPK-VSEKTKLNNPVPVATNSFRAMP 77
 QY 76 NLHLLIVNNKISKVSFGATPLVYKLERLYLSKNQKLEPEKMPKTYOELR--AHNEI 132
 Db 78 NLVSLHGHQIRVAVAGARGLKQLYVLSHNDIVLAGAFDDLTETLYLIDNNKV 137
 QY 133 TVKRYTFNGLQMWIVLELGTNPDKSSGIEGAFQKMKLSYRIADTNITSTIQG--- 189
 Db 138 TELPRGLSLPLVLMFIQLNKKIRE--LMSGAFQAKDLRLVLSNSSLQPGALDD 195
 QY 190 PPSITELHLDQNKISRVDASLKLGNLNLAKLGLSPNSISAV--DNGSLANTPHLEHLDD 248
 Db 196 VENLAKYVLRNQLSSYPSALSRLRYVELKLSHNLKSI PDNAFQSPGRVYETLWLDN 255
 QY 249 NKLTRV--PGGLAEKRYIOVYVTLHNNNISVVGSSDFCPGHNTKASVSGVLSFNPQYW 307
 Db 256 TNLKPSDGAFLVYTLAKVHLNNRLHQLP-----NFPDSLETTLTNP---W 304
 QY 308 E-----IOPTFRCYVVR 320
 Db 305 KCTCQLRLRLRLWLEAKTSRPDATCASPAKRGQHIR 340

RESULT 25
 A58532
 glial cell membrane glycoprotein LIG-1 precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
 C/Accession: A58532
 R/Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaoka, A.; Takagi, T.
 J. Biol. Chem. 271, 22522-22527, 1996
 A/Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically
 A/Reference number: A58532; MUID:96394333; PMID:8798419
 A/Accession: A58532
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1091 <SUZ>
 A/Cross-references: GB:D78572; NID:91545806; PID:BA11416.1; PID:91545807
 C/Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-1
 F:36-61/Domain: proteoglycan amino-terminal homology <PA>
 F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F:99-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR1>
 F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR2>
 F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR3>
 F:385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR4>
 F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR5>
 F:440-485/Domain: proteoglycan carboxy1-terminal homology <PCH>

Query Match	17.0%;	Score 291;	DB 2;	Length 1091;
Best Local Similarity	30.7%;	Pred. No. 3.6e-13;		
Matches 84; Conservative	55;	Mismatches 121;	Indels 14;	Gaps 8;

```

QY      24 CFFRCQCHIRVAVOCSSLDGDKVPRDLPBDTLLLDLONNKKTTEKQGFKULKYIHLIIV  83
Db      43 CAAACTCAANSIDSCSGLATLPRDLPSWTRISLNTSYNRSLSEIDSAFEDULTQGEVYLN  102
QY      84 NKKISKVSGATPLPYKLERLYVSKQOLKELPERMKP--TLOELRAHENEITKVRKVF  140
Db      103 SNEI:PAI-PSLGTASIGVAVSLFLQHNKIKSLVSDSCSKSYSLSEVLDLSSNNITEISSCF  161
QY      141 -NGLNQWITYIEGTNPDLKSSGAINGAPQGW-KLGSYRIADITNITSPOGL--PSSLTEL  166
Db      152 PFGLR---IRELTASNRSISLESQAFDLSRSLITRLSKNRITQIPVAFKLPRIITOL  218
QY      197 HLDGKISRVDAASLKGILNNTAKLGLSFNSISAVDNGSLANTPHLRHLDNKKLTFV-P  255
Db      219 DLRNRRIIRLIEGLTFQGLDSLLEVLRLORNNTISLTDQAFWGLSKMHVLIHLEVNSLVEVNS  278
QY      256 GGLAEHKYIQVYVYIHNNTISVSVSS--DPCPPGH  287
Db      279 GSLYGLTALHQLNNTNISRIORDQMGSPQCKIILH  312

```

RESULT 26

G protein-coupled receptor FEX - mouse
 G.Species: Mus musculus (house mouse)
 C.Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
 C.Accession: UG0193
 R.Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
 Biochem. Biophys. Res. Commun. 254, 273-279, 1999
 A.Title: Identification of a novel, seven-transmembrane receptor with homology to glycophorin A
 A.Reference number: UG0193; PMID:99121227; PMID:9920770

Query Match: 16.7%; Score 285.5; DB 2; Length 907;

```

QY 24 CFFRCOCHL -RV---VOCSDJGLDGVDPDI,PPDTLLDLONNKJTEIDGQFXYLNKH 78
Db 34 CSHCHCEJDEKMLLRVDCSDJGLSEBPNLSVFTSYLDLNNNTISQLPASLLHRCFLB 93
QY 79 ALIYNNKISKVSPGAFPLVYKLERLYSKNOJ,KEJ,PERK---PKTQELRAHENEITKY 135
Db 94 EIRLGNALTTI,PKGAFPTGLHSIKVLMLQNNOLRKVEBALQNLRSJGLRUDANHISVY 153
QY 136 RAYTPAGLNMIVIELGTNTPKSSGJENAFQCMKGLSTIRADNTYTSIPQ---GLPPS 192
Db 154 PPSCSGSLSHLHMLDDNALTDVPQO -AFRSLSLQAMTLANKIHIIADYAFENUSS 211
QY 193 LTELHLDGNKISRVDAAISLKGJLNTLAKJGLSPENSIAVNGSILANTPHREJLHNNKLT 252
Db 212 LVVTLHNNRIRHSIGKCFDGLHSFETLPLDNNNDEBPT -AKITLSNJKELGFSNNIR 270
QY 253 RYPGGLAEHYIQ-----VYTLANNNTISVSSDF 282
Db 271 SIP---ERAFVGNBSLITIHFYDNDIQVGVSAF 301

```

RESULT 27

neuronal leucine-rich repeat protein-3 - rat
JC7763
C/Species: Rattus norvegicus (Norway rat) 1st 2000 About 3000

Query Match	16.5%;	Score 283.5;	DB 2;	Length 707;
Best Local Similarity	28.4%;	Pred. No. 6.9e-13;		
Matches	99;	Conservative	52;	Mismatches 126;
			Indels	71;
			Gaps	13;

[illegible]

RESULT 28

insulin-like growth factor acid-labile chain - baboon
 C|Species: Papio sp. (baboon)
 C|Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C|Accession: JCS239
 R|Delahanty, P.; Baxter, R.C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A|Title: The cloning and expression of the baboon acid-labile subunit of the insulin-
 A|Reference number: JCS239; MUID:97040714; PMID:8886027

Query Match	15.9%	Score 273	DB 2	Length 605
Best Local Similarity	25.9%	Pred. No. 3.3e-12		
Matches 87; Conservative		58; Mismatches 139	Indels 52;	Gaps 9;

QY 5 GIGPEVDDRRDEPESLGPVCPRCQC-----HNRVQCSDLGLDKVPKXLPPTDTLLDL 58
| | : | | | : | | : | |
DB 27 GAEPGTGEAL-----GPACRATCACSYDDEVNELSVFCSSRNLTRLPDGIPGGTQALWL 81

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 09:36:44 / Search time 84 Seconds
(without alignments)
1010.706 Million cell updates/sec

Title: US-10-004-176-6

Sequence: 1 VASASGIGPEVPDDRPFEPSEL.....QPSTFCVYRSAGIOLGNVK 329

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvtnus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1229	71.7	359	13 Q9DE03	Q9de03 oreochromis
2	895.5	52.3	410	13 Q9DD27	Q9dd27 petromyzon
3	894.5	52.2	310	13 Q9DD28	Q9dd28 petromyzon
4	887.5	51.8	347	13 Q9DE00	Q9de00 petromyzon
5	883.5	51.6	370	13 Q9DE04	Q9de04 oreochromis
6	878.5	51.3	388	13 Q9DD29	Q9dd29 petromyzon
7	817.5	47.7	325	4 Q8NAB7	Q8nab7 homo sapien
8	784	45.8	224	13 Q9DE01	Q9de01 brachydanio
9	548.5	32.0	187	4 Q9NXP3	Q9npx3 homo sapien
10	487	28.4	96	11 Q63156	Q63156 rattus norv
11	385.5	22.5	378	11 Q8CAZ9	Q8caz9 mus musculu
12	342	20.0	627	4 Q8NC95	Q8nc95 homo sapien
13	341	19.9	649	11 Q8BGT1	Q8bgt1 mus musculu
14	334.5	19.5	1534	4 Q75093	Q75093 homo sapien
15	334.5	19.5	1618	4 Q9UL17	Q9ul17 homo sapien
16	332	19.4	674	4 Q8WVA2	Q8wva2 homo sapien

17	330	19.3	120	13 Q9DE02	Q9de02 brachydanio
18	328.5	19.2	1531	11 Q9WV55	Q9wv55 mus musculu
19	328	19.1	1523	11 Q9WV4	Q9wv4 mus musculu
20	327.5	19.1	1531	11 Q88279	Q88279 rattus norv
21	327	19.1	1523	11 Q88280	Q88280 rattus norv
22	325	19.0	1440	5 Q20204	Q20204 caenorhabdi
23	325	19.0	1512	13 Q9DE36	Q9de36 brachydanio
24	325	19.0	1523	4 Q75094	Q75094 homo sapien
25	324.5	18.9	1474	11 Q8CUG9	Q8cig9 rattus norv
26	323.5	18.9	1458	11 Q8CUG8	Q8cig8 rattus norv
27	322	18.8	1529	4 Q94813	Q94813 homo sapien
28	321.5	18.8	376	4 Q81V47	Q81v47 homo sapien
29	318.5	18.6	1515	13 Q9DE37	Q9de37 brachydanio
30	318	18.6	1521	11 Q9R1B9	Q9r1b9 mus musculu
31	317	18.5	1525	4 Q9Y507	Q9y507 homo sapien
32	316.5	18.5	1530	11 Q9WU55	Q9wu55 rattus norv
33	316	18.4	1530	13 Q9WU23	Q9wu23 xenopus lae
34	315	18.4	1521	4 Q95710	Q95710 homo sapien
35	314	18.3	1025	11 Q9Z166	Q9z166 mus musculu
36	313	18.3	1095	13 Q90XG4	Q90xg4 gallus gall
37	312.5	18.2	798	4 Q8WV22	Q8wv22 homo sapien
38	309.5	18.1	796	11 Q8WV21	Q8wv21 mus musculu
39	309.5	18.1	796	11 Q8WV21	Q8wv21 rattus norv
40	307.5	18.0	1346	5 Q9V477	Q9v477 dirosophila
41	307	17.9	396	11 Q8C3D9	Q8c3d9 mus musculu
42	303.5	17.7	652	11 Q99PH1	Q99ph1 mus musculu
43	303.5	17.7	653	4 Q9HBM1	Q9hbm1 homo sapien
44	302.5	17.7	406	11 Q8CJ10	Q8cj10 rattus norv
45	302	17.6	640	4 Q9HCJ2	Q9hcj2 homo sapien

ALIGNMENTS

RESULT 1

Q9DE03 PRELIMINARY; PRT; 359 AA.
AC Q9DE03;
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 23, Last annotation update)
DE Decortin.
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.,
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247822; AAG40157.1; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003581; LRR_Typ.
DR Pfam; PF00560; LRR_7.
DR Pfam; PF01462; LRRNT_1.
DR SMART; SMO0013; LRRNT_1.
DR SMART; SMO0369; LRR_Typ_1.
DR PROSITE; PSS0506; LRR_TYPICL; 2.
SQ SEQUENCE 359 AA; 39807 MW; F19F9MAAE7572C6 CRC64;

Query Match

Best Local Similarity 71.7%; Score 1229; DB 13; Length 359;
Matches 229; Conservative 46; Mismatches 53; Indels 2; Gaps 2;

QY 1 VASASGIGPEVPDDRPFEPSEL-GVPCPRQCCHLRVQCSDLGLDKVPHLPPDTTLTDQ 59
DB 29 MEDSGSGPVETS-PLPVTGSGPKCFRCQCHLRVQCSDLGLKAVPBDIPDPTTLTDQ 87

Qy	60	NNKITTEKRODPFNLKNTLALILVNNKSKVSPGAFTEVLVYLBRYLXSKOULEPERMP	112
Db	88	NNKITTEKENDPFNLGJHALILVNNKLTTHPKAFSPYTKQRYLXSKLLKJEMPMNP	147
Qy	120	KTLQELRAHENETTKVRKVTENGJNOMVIELGTNPXSGIENGAFQGMKLSYIRIAD	179
Db	148	KSIOELRIHENETTKKKKASFOGMSHVIVMEJGSNPLTKAGIEAGAFADLRKASYIRIAD	207
Qy	180	TNITSIPQGLPEBLTETELHDGKNISPVDAASLKGJLNNLAKIGLSNGLSANDNSLANTP	239
Db	208	TNITEVPKGPSSLSLEHLHDGNKITKLTADRKGMKNLAKIGLSNQISVENSTLISNAP	267
Qy	240	HLREHLDDNNKLTTRVPGGLAEHKYIQVYVLAHNNNISVYSSDPFCPBGHNTKKASVGSYL	299
Db	268	HLREHLDDNNALTSVPPGLPDRHKYIQVYVLAHAKIAAVGTEDFCPBGHNTKKANYSIGSL	327
Qy	300	FSNPVQYVMELOPSTFPCVYVRSALIQGNK 329	
Db	328	FSNEVPYMEVOPVTFRCVFDRSALIQGNR 357	

RESULT 2			
Q9DDZ7			
ID	Q9DDZ7	PRELIMINARY;	PRT; 410 AA.
AC	Q9DDZ7;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Bağlycan-like protein 2.		
GN	BGL2.		
OS	Petromyzon marinus (Sea lamprey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;		
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.		
OX	NCBI_taxid=7757;		

RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; Pubmed=11040287;
RA Shitucani S., Sato A., Toyosawa S., O'nigin C., Klein J.;
RT "J.Mol. Evol.51:363-373(2000).
RL EMBL; AF247828; AAC40163.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT_1
DR PROSITE; PS50506; LRR_TYPICAL; 2.
SQ SEQUENCE 410 AA; 44671 MW; 3EC96E9A90BFCFEA CRC64;

Query Match	52.3%	Score	895.5	DB	13	Length	410
Best Local Similarity	53.6%	Pred.	No. 2.4e-54				
Matches	173	Conservative	51	Mismatches	90	Indels	9
						Gaps	2

QY	8	PEVDDDDDFEBSLAPWCFEFCOCHLRVQCSJDLGDKRPKDPPRTLLDLONNKITEIK	67
Db	95	PPPPDAS-----CFEGCQCSARVQCSJDLGVSVPQALPKDARILLDLONNKITEIK	146
QY	68	DGDPRKLNKHALILVNKKISKVSPGAFPIVKEERLYISKQOLKEPKNPKITLOELRA	127
Db	147	QODEKKGANKRYALVALVNNLISKHAPAFAPLSLIDLXISHQOLTEVWGSPSSLVEIRI	206
QY	128	HENETIVKRYKTEPYGLNOMIVIELGPNPLKSSGIEKNGAFQMKKISYRIDPNTITSIQ	187
Db	207	HENNIIKKIKPDABSGMKRLHALEKGNPLDSTIEGAEGERLYAVRVSSKARIPEK	266
QY	188	GLPESLTELHDGKNSIRVDAASLUKGINLAKLGSFNSISAVDNGSIANTPHIRELHD	247
Db	267	DLPSNIOELHLENHQITALEGBDLIRYPLIHRGLGSYNQIKYIQNGSLETCCHIRELHD	326
QY	248	NNKILTRVPGSLAEHKITQVYLLHNNNISVVGSSDFCPPEGHNTKKASYSVGSJESNPVOYW	307
Db	327	SNVLTQVPEGLATFKHLQVYLLHNNKIAAKYKSDDFCSKASAPKRVLYSGSILFNDPVAWY	386

QY 308 EIQPSTFRCVVRSALQLG-NYK 3225
::| | | | | | | |
Db 387 DVPSAFCRCVASRSAVQFSQNFR 4095

RESULT 3	Q9DDZ8	PRELIMINARY;	PRT;	310 AA.
ID	Q9DDZ8			
AC	Q9DDZ8;			
DT	01-MAR-2001 (TREMBlrel. 16, Created)			
DT	01-MAR-2001 (TREMBlrel. 16, last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, last annotation update)			
DE	Baglycan-like protein 2 (Frigment).			
GN	Bgl2.			
OS	Petromyzon marinus (Sea lamprey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;			
CC	Petromyzontiformes; Petromyzontidae; Petromyzon.			
OX	NCBI_TaxID=7757;			

RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., Ohnigin C., Klein J.,
RT "Blygcan-like extracellular matrix genes of agnathans and teleosts."
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247827; AAC40162.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR_7.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PSS0506; LRR_TYPICAL; 2.
FT NON_TER 1 1
SQ SEQUENCE 310 AA; 34572 MW; 6FB8E05B14339EF5 CRC64;

Query Match	52.2%	Score 894.5	DB 13	Length 310
Best Local Similarly	55.4%	Pred. No. 1.9e-54		
Matches 170	Conservative 51	Mismatches 85	Indels 1	Gaps 1

ID	Q9DE00	PRELIMINARY;	PRT;	347 AA.
DT	01-MAR-2001	(TrEMBLrel. 16,	Created)	
DT	01-MAR-2001	(TrEMBLrel. 16,	Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23,	Last annotation update)	
DE	B1g1ycan-like protein 1 (Fragment).			

GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OC NCBI_TaxID=7757;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247825; AAG40160.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR_8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
FT NON TER 1
SQ SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 51.8%; Score 887.5; DB 13; Length 347;
Best Local Similarity 54.4%; Pred. No. 6.9e-54;
Matches 178; Conservative 50; Mismatches 90; Indels 9; Gaps 3;

Qy 4 SGIGPEVDDRDPEPSIGPVCPRQCHLRVVGCSDLGLDKVPCDLPPTLLDLONNKI 63
Db 28 SPVAPPPQ-----PSVG--CPFGQCSLRVVGCSDLGLKSPASIPDAMVLDQSNKI 79
Qy 64 TEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMKXTLQ 123
Db 80 TEIKQDPEKGLAQHAFVNVNLLAKIHPKAFAPVVSIDKLYISNRLTEVPTGISPLI 139
Qy 124 ELRAHEKITVRYKTYENGLOMYIELGTNPLKSSGIEGNGAFQGMKLSYRIADTNIT 183
Db 140 ELRAHEMLIKKVPKDTFNNQQLHVLIELGKNPLSSGIEVGAFNGLDLTYIRISYSKLT 199
Qy 184 SIPOGLPSTLTELHDGKISRVDASLKGNNLAKLGSFNSISAVNGSLANTPHIRE 243
Db 200 QLPKELPSTLTELHGEHEIYALIEDEDLPGRPYLFRGLSTNKTTEVNGSLAVSGLIRE 259
Qy 244 LHLNNKLTTRVPGGLAEHKYIQVYVLIANNNISVVGSSDFCPGHNTKASYSVSLFSPN 303
Db 260 LHLNNLTVSPPGSLKRSILNVYLIHNSKIKKVKPTDFCPTVSPKQAQYAGISLYNRP 319
Qy 304 VQWEIQSTFRCYVRSALQIG-NYK 329
Db 320 VKYWEVPPSPVRCVANHNAIHFGSNYR 346

RESULT 5
Q9DE04 PRELIMINARY; PRT; 370 AA.
ID Q9DE04;
AC Q9DE04;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Biglycan-like protein 3.
GN BGL3.
OS Oreocheilus niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Cichlidae; Oreocheilids.
OC NCBI_TaxID=8128;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247821; AAG40156.1; -.
SQ SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

DR InterPro; IPR001611; LRR.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR_9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 2.
SQ SEQUENCE 370 AA; 42177 MW; BCD0675694ECA287 CRC64;

Query Match 51.6%; Score 883.5; DB 13; Length 370;
Best Local Similarity 53.0%; Pred. No. 1.4e-53;
Matches 170; Conservative 53; Mismatches 97; Indels 1; Gaps 1;

Qy 9 EVPPDRDFEPELIGVCPFCRQCHLRVVGCSDLGLDKVPCDLPPTLLDLONNKITEIKD 68
Db 50 EVDDDDDDDDVNDDECAHCHSPRVVQCSIQGLISVPDKIPBTVMIDLQNDITELQ 109
Qy 69 GDFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMKXTLQELRAH 128
Db 110 DDFGLNKLVLFLNNKISRHPKAFKNNMDLRLYLSYMLNIPANLPNVTELRPH 169
Qy 129 ENETTKRKYTFNGLNOMIVIELGTNPLKSSGIEGNGAFQGMKLSYRIADTNITSIQ 188
Db 170 ENQIDRQKQAFKGLRKLHVLGAMPLVNSGIEIGAFNGISTL-YIGIAEAKLTSPKD 228
Qy 189 LPSLTTELHDGKISRVDASLKGNNLAKLGSFNSISAVNGSLANTPHIRELHDN 248
Db 229 FPSITLSDLYNKISKVEIDFIRYKNLQRLGAFNQIKYVNGSLANTKIKETIYIDN 288
Qy 249 NKLTRVPGGLAEHKYIQVYVLIANNNISVVGSSDFCPGHNTKASYSVSLFSPVQWE 308
Db 289 NRMKVPVPGSLSLRYQYIFLHGKISVGINDCPIRADSKNPYTGISLPAFVKYWA 348
Qy 309 IQPSTFRCYVRSALQIG-NYK 329
Db 349 IQPATFRCYTRRGVQGNFR 369

RESULT 6
Q9DD29 PRELIMINARY; PRT; 388 AA.
ID Q9DD29;
AC Q9DD29;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Biglycan-like protein 1 (Fragment).
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OC NCBI_TaxID=7757;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247826; AAG40161.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR_8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
FT NON TER 1
SQ SEQUENCE 388 AA; 42542 MW; 2E07169E9BB6071B CRC64;

Query Match 51.3%; Score 878.5; DB 13; Length 388;
Best Local Similarity 53.8%; Pred. No. 3.4e-53;
Matches 176; Conservative 52; Mismatches 90; Indels 9; Gaps 3;

Qy 4 SGIGPEVDDRDPEPSIGPVCPRQCHLRVVGCSDLGLDKVPCDLPPTLLDLONNKI 63

```

Db      69  SEVADPEP-----PSVG--CFEGCCCSIRVVOCSDLGLKSVAPGIPKARAVLDQSNKI 120
Qy      64  TEIKQDGFNLKNTLHALLIVNNKISKVSBCAFTPLVKERLYLSKQKLEPERKPKTIQ 123
Db      121  TEIKQDGFGLAQOLHALLIVNNLILAKIHPKAPAPWSDLKLYISHRLTEVPTGPEPSLI 180
Qy      124  ELRAHENEITTKYKATFENGANOMIVIELGTNPILKSSGIEGNGAFQGGKLSYRIADTNT 183
Db      181  ELRAHENEILKRVKPTFIINNGRLHVLKQKPLPSSGIEVGAFNGLDKTYIRISIKLT 240
Qy      184  STPQGLPSLTLELHLDGKTKISRVDAASLKLNNLAKLGSFNSISAVNGSLANTPHLRE 243
Db      241  QLPKELPNSILTEHLEEGNEIIVAIIEEDLFGYPLYFLGLGSYNKITEVQNGSLAVSGNLE 300
Qy      244  LHLNNKLTRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLFSP 303
Db      301  LHLNNLIVSPPGSLKSLNVLVHNSKIREVKPTDFPTVPSPKAQAQYAGISLYDNP 360
Qy      304  VQYWEIOPSTFRVCYVRSALIQG-NYK 329
Db      361  VQYWEVPSVFRVCVNNHAIHFGSNR 387

```

RESULT 7

```

Q9NAB7  ID  Q9NAB7  PRELIMINARY;  PRT;  325 AA.
AC  Q9NAB7:
DT  01-OCT-2002 (TREMBlrel. 22, Created)
DT  01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
OS  Hypochemical protein FLJ35635.
OC  Homo sapiens (Human).
OC  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC  NCBI_TaxID=9606;
RN  NCBI_TaxID=9606;
RP  SEQUENCE FROM N.A.
RC  TISSUE=Splice;
RA  Houtua T., Hiraoka S., Yoshida M., Watanabe S., Ishida S., Ono Y.,
RA  Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA  Sugiyama T., Irie R., Otsuki T., Sato H., Oca T., Wakamatsu A.,
RA  Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA  Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA  Magatsuna M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA  Suzuki Y., Sugano S., Negahari K., Maehuo Y., Nagai K., Isogai T.;
RT  "NEO human cDNA sequencing project."
RT  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AK092954; BAC04007.1; -.
DR  InterPro; IPR000372; LRR_Nterm.
DR  InterPro; IPR003591; LRR_cyp.
DR  Pfam; PF01462; LRRNT; 1.
DR  SMART; SM00013; LRRNT; 1.
DR  PROSITE; PS50506; LRR_TYPICAL; 2.
KW  Hypochemical protein.
SQ  SEQUENCE 325 AA; 36637 MW; 33BAC7DEB17982BE CRC64;

```

Query Match 47.7%; Score 817.5; DB 4; Length 325;
 Best Local Similarity 49.8%; Pred. No. 4,6e-49;
 Matches 164; Conservative 40; Mismatches 80; Indels 45; Gaps 3;

```

Qy      2  EASGIGPE-VPPDRDPEPSLGPVCPRCOCHLRVVOCSDLGLDKVPKDLPPPTLLDLCN 60
Db      40  EASGADTSGVLDPSVTPYSAMCPGCHLRVVOCSDLGLKSVKELISPTLLDLCN-98
Qy      61  NKITEIKQDGFNLKNTLHALLIVNNKISKVSBCAFTPLVKERLYLSKQKLEPERKPK 120
Db      99  -----KLYSKNHLVLEIPNPLS 116
Qy      121  TLQELRAHENEITTKYKATFENGANOMIVIELGTNPILKSSGIEGNGAFQGGKLSYRIADT 180
Db      117  SLVEELRIHNRIRKYKGVFSGLRNNNCIEMGNGPLENGFEPGAFDGH-KINYIRISBA 175

```

```

Qy      181  NTSIPQGLPSLTLELHLDGKTKISRVDAASLKLNNLAKLGSFNSISAVNGSLANTPH 240
Db      176  KLTGIPKDLPETLNLHLDGKTKISRVDAASLKLNNLAKLGSFNSISAVNGSLANTPH 235
Qy      241  LRELHLDNNKLTRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLF 300
Db      226  LRELHLDNNKLARVPSGLPDLKLGVLVHNSNITKVGVDNCPGPGKRAYNGISLFL 295
Qy      301  SNPVQYWEIOPSTFRVCYVRSALIQGNTK 329
Db      296  NNPVQYWEVOPATFRCVTRALIQPNYK 324

```

RESULT 8

```

Q9DE01  ID  Q9DE01  PRELIMINARY;  PRT;  224 AA.
AC  Q9DE01:
DT  01-MAR-2001 (TREMBlrel. 16, Created)
DT  01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
OS  Decodon (Fragment).
OC  Brachydanio rerio (zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OC  NCBI_TaxID=7955;
RN  NCBI_TaxID=7955;
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20496956; PubMed=11040287;
RA  Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT  "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RT  J. Mol. Evol. 51:363-373 (2000).
DR  EMBL; AF247824; AAG40159.1; -.
DR  ZFIN; ZDB-GENE-010102-1; dcn.
DR  InterPro; IPR001611; LRR.
DR  InterPro; IPR003591; LRR_cyp.
DR  Pfam; PF00560; LRR; 7.
DR  SMART; SM00369; LRR_TYP; 1.
DR  PROSITE; PS50506; LRR_TYPICAL; 2.
FT  NON_TER 1
FT  NON_TER 1
SQ  SEQUENCE 224 AA; 24442 MW; 54A1B7AB91667DF0 CRC64;

```

Query Match 45.8%; Score 784; DB 13; Length 224;
 Best Local Similarity 68.9%; Pred. No. 6,1e-47;
 Matches 153; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

```

Qy      45  VPKDLPPPTLLDLCNNKITEIKQDGFNLKNTLHALLIVNNKISKVSBCAFTPLVKERL 104
Db      3  VPEKIPPLPTLLDLCNNKITEIKENDPFGKLGLOTLIVNNKITYIHAKAFSLINLEL 62
Qy      105  YLSKNQKLEPERKPKTIQELRAHENEITTKYKATFENGANOMIVIELGTNPILKSSGIEG 164
Db      63  YLSKNLKEVPANIPKSIQELRIHENQINKIKKSFPAKAVIWEISNPLSSGVDNG 122
Qy      165  AFQGGKLSYRIADTNTITSIPQGLPSLTLELHLDGKTKISRVDAASLKLNNLAKLGSF 224
Db      123  AFADLKRVSAIRIADTNTISIPKGLPSSLFEHLHDGKTKITKTVAOSLKLKSLGLSH 182
Qy      225  NSISAVNGSLANTPHLRELHLDNNKLTRVPGGLAEHNTYIOV 266
Db      183  NEISVENGSLANVPHRELHLDNNALYAVPGLADHNTYIOV 224

```

RESULT 9

```

Q9NXP3  ID  Q9NXP3  PRELIMINARY;  PRT;  187 AA.
AC  Q9NXP3:
DT  01-OCT-2000 (TREMBlrel. 15, Created)
DT  01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE  01-MAR-2003 (TREMBlrel. 23, Last annotation update)

```

DE Hypothetical protein FLJ20129.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Oca T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK000136; BAA0967.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003591; LRR_TYP.
 DR Pfam: PF00560; LRR; 3.
 DR PROSITE: PS50506; LRR_TYPICAL; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;

Query Match 32.0%; Score 548.5; DB 4; Length 187;
 Best Local Similarity 53.2%; Pred. No. 1.1e-30;
 Matches 99; Conservative 42; Mismatches 44; Indels 1; Gaps 1;

QY 143 INOMVIELGTPTLKSSGIENGAFQGMKKLSYIRIADNTITISPGGLPSLTLEHLDGKX 202
 DB 1 MNAHLVLEKSNAPLNDNNGIEPGAFEGV-TVFIRIAEAKLISVPGKPLETLEHLDYK 59
 QY 203 ISRVDAASIKGLNNTAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTVPVGLAEHK 262
 DB 60 ISTVELDEPKRYKELQRLGLGNKKITDIENGSLANIPRYEHLNENKTKIPSGLEPK 119
 QY 263 YIQVYVYHNNISVYSSDFPCPGHATKASISGSLSENPQYMEIQSTRCYVYMSA 322
 DB 120 YIQIIFLHNSISARVAVDPCTVPKMKSLYSALSFPNNPKYEMOPATERCVLSRMS 179
 QY 323 IQLNNY 328
 DB 180 VOLGNP 185

RESULT 10

063156 PRELIMINARY; PRT; 96 AA.

AC 063156; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Decorin (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RA Moates-Staats B.M., Stiles A.D., Xu L.;
 RT "Expression of decorin RNA in rat lung undergoing chronic lung
 injury."
 RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L75825; AAA85371.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003591; LRR_TYP.
 DR Pfam: PF00560; LRR; 3.
 DR PROSITE: PS50506; LRR_TYPICAL; 1.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10398 MW; C6D19F1750B050D0 CRC64;

Query Match 28.4%; Score 487; DB 11; Length 96;
 Best Local Similarity 100.0%; Pred. No. 9e-27;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 YIRIADNTITISPGGLPSLTLEHLDGKISRVDASIKGLNNTAKLGLSFNSISAVDNG 233
 DB 1 YIRIADNTITISPGGLPSLTLEHLDGKISRVDASIKGLNNTAKLGLSFNSISAVDNG 60
 QY 234 SLANTPHLRELHLDNNKLTVPVGLAEHKYIQVYVL 269
 DB 61 SLANTPHLRELHLDNNKLTVPVGLAEHKYIQVYVL 96

RESULT 11

08CA29 PRELIMINARY; PRT; 378 AA.

AC 08CA29; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Proline arginine-rich end leucine-rich repeat.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL: AK037150; BAC29722.1; -
 SQ SEQUENCE 378 AA; 43293 MW; 6F85A1B935FFB8C CRC64;

Query Match 22.5%; Score 385.5; DB 11; Length 378;
 Best Local Similarity 32.2%; Pred. No. 6e-19;
 Matches 93; Conservative 57; Mismatches 124; Indels 15; Gaps 6;

QY 2 EASGIGPEVPDRDRPEPSLGVPCCPC--HLRVQCSLDGLDKVKDLPDPTLLDL 58
 DB 50 EPTDLPPLPPG--PSSVFPCPCRECYCPDPFSPALCDSRNLRVSV-IPRTHYLYL 105
 QY 59 QNNKITEIKDGFKULKULHALIVNNKISKVSPGAPFLVLELYLTKNQLKEPEKM 118
 DB 106 QNNFTTEPLPSFGVATGLRWVNDNNRIKRVQDQVGLKLSLATLEKQLEVPSSAL 165
 QY 119 PRTLOELRAHNEITKRVKTFNGINQMIIVIELGTPPLKSSGIENGAFQGMKKLSYIRIA 178
 DB 166 PRNLEQLSLQNLISRIIPGVPSKLEMLLDLDQNNRLSDGVFKADTFQGLKNLQNLIA 225
 QY 179 DTNITSITQGLPPSLTEIHLGDKTISRVDASIKGLNNTAKLGLSFNSISAVDNGSLANT 238
 DB 226 HNIILKMPKPKVQALHQLYLSNKTETIPNGYFDPFPLAIRMYNVLDS--DRGLPRNS 283
 QY 239 ---PHLRELHLDNNKLTVPVGLAEHKYIQVYVYHNNISVYSSDFPC 284
 DB 284 FDISNLVLVLSHNNKISNP--ALSNDLHILNNSIEKINGIQIOP 329

RESULT 12

08NC95 PRELIMINARY; PRT; 627 AA.

AC 08NC95; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90402.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match	20.0%;	Score 342;	DB 4;	Length 627;
Best Local Similarity	31.9%;	Pred. No. 1.2e-15;		
Matches 90;	Conservative 49;	Mismatches 85;	Indels 58;	Gaps 9

RESULT 13	
008G71	
ID	PRELIMINARY; PRT; 649 AA.
AC	008G71;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE	Fibronectin leucine rich transmembrane protein 3 homolog.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Head; and Testis;
RX	MEDLINE=22354683; PubMed=12466851; and
RA	The FANTOM Consortium.
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RL	60,770 full-length cDNAs.";
DR	Nature 420:563-573 (2002).
DR	EMBL; AK028252; BAC25843.1; -;
DR	EMBL; AK031464; BAC27417.1; -;

Db 245 PGTSRLKLYLQDNHINRVPPN--AFSYLRQLYRLDMSNNNLS 284

	RESULT 14		
	075093		
ID	075093	PRELIMINARY;	PRT; 1534 AA.
AC	075093;		
DT	01-NOV-1998	(TRMBLrel. 08, Created)	
DT	01-AUG-1999	(TRMBLrel. 11, Last sequence update)	
DT	01-MAR-2003	(TRMBLrel. 23, Last annotation update)	
DE	SULT-1 protein.		
CN	SULT-1.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99033071; PubMed=9813312;		
RA	Itch A., Miyabayashi T., Ohno M., Sakano S.;		
RT	"Cloning and expressions of three mammalian homologues of dirosophila		
RT	silt suggest possible roles for silt in the formation and maintenance		
RL	of the nervous system.";		
RL	Brain Res. Mol. Brain Res. 62:175-186(1998).		
DR	EMBL; AB017167; BAA5184.1; -.		
DR	HSSP; P00743; ICCF.		
DR	InterPro; IPR000152; Asx_hydroxyl_1.		
DR	InterPro; IPR006207; Cys_knot_C.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR003645; FOLN.		
DR	InterPro; IPR002049; Laminin_EGF.		
DR	InterPro; IPR001791; Laminin_G.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR000372; LRR_Nterm.		
DR	InterPro; IPR003591; LRR_typ.		
DR	pfam; PF00008; EGF_9.		
DR	pfam; PF00054; laminin_G; 1.		
DR	pfam; PF00560; LRR_19.		
DR	pfam; PF01463; LRCT; 4.		
DR	pfam; PF01462; LRNT; 4.		
DR	PRINTS; PR00011; EGF_LAMININ.		
DR	SMART; SMART0041; CT; 1.		
DR	SMART; SMART0179; EGF_CA; 2.		
DR	SMART; SMART0274; FOLN; 3.		
DR	SMART; SMART0282; LamG; 1.		
DR	SMART; SMART0082; LRCT; 4.		

DR SMART; SM00013; LRNT; 4.
 DR SMART; SM00369; LRR_TYP; 10.
 DR PROSITE; PS0010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS00022; EGF_1; 9.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
 DR PROSITE; PS50506; LRR_TYPICAL; 5.
 DR EGF-like domain.
 KW EGF-like domain.
 SQ SEQUENCE 1534 AA; 167952 MW; 8954EPBEADAEBA1 CRC64;
 Query Match 19.5%; Score 334.5; DB 4; Length 1534;
 Best Local Similarity 25.1%; Pred. No. 1.3e-14;
 Matches 97; Conservative 65; Mismatches 121; Indels 103; Gaps 9;
 QY 10 VPDRDF---EPSPGVPFRCQCHLRYVOCSDLGDKVPRKDPDPTLLDLONNKITE 65
 DB 495 IPGTEDYQINSECNSDVVCPEKRCCEANVVECSSIKLTKEIPERIPQSTAEIRLNNEISI 554
 QY 66 IK-DGDFPKLKNLHALILVNNKISKVSPGAFPLVKLERLYLSKNQLKELEPKPKTQE 124
 DB 555 LEATGMFKLTHLKKNLSNNKVSIEIDGAFEGAASVELHTANQLSISGMRGLDG 614
 QY 125 LRA---HNEITKYKVTENGINQIVIELGTNPDKSGIENGAFQGMKKLS----- 173
 DB 615 LRTMLRNRRISCIHNSFTGLRVRLSLYDNOITT--VSPGAFDTLQSLSTINLAMP 672
 QY 174 ----- 173
 DB 673 FNCNQCLAMLGWLRRKRIYVGNPRCONPDLRQIPLODVAFPDFRCEGEGGCLPRP 732
 QY 174 -----YIRIADNITSIPQGLPPSLTELHLDNKISRDAASLKGNNLAKGL 222
 DB 733 QCPQECACLDIVVRCNSNHLALPKGIPKNTVELYLDNQFTLV-PQLSTFKYIQVLDL 791
 QY 223 SFNSISAVNGSLANTPHLREHLDNKLTRVP---GGLAEHKYIOVYVYLNHNISVYG 278
 DB 792 SNNKISSLSNSSFNNMSQTLTLLSYNALQCIPLAFGL---RSLRLSLHGNDISTLQ 848
 QY 279 SSDFCPPGHNTKKASYSGVSLFSNPV 304
 DB 849 EGIF-----ADVTSLSHLAIGANPL 868
 RESULT 15
 Q9U1L7 PRELIMINARY; PRT; 1618 AA.
 AC Q9U1L7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE MEGP4 (Fragment).
 GN MEGP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98360089; PubMed=9693030;
 RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
 RT "Identification of high-molecular-weight proteins with multiple EGF-
 like motifs by motif-trap screening."
 RL Genomics 51:27-34(1998).
 DR EMBL; AB011537; BAA32465.3; --
 DR HSSP; P00743; ICGP.
 DR Genew; HGNC:11085; SLIT1.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_III.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00008; EGF_9.
 DR Pfam; PF00054; Laminin_G; 1.
 DR Pfam; PF00560; LRR; 19.
 DR Pfam; PF01463; LRCT; 4.
 DR Pfam; PF01462; LRNT; 4.
 DR PRINTS; PR00010; EGFBLDOD.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR SMART; SM00282; Lmg; 1.
 DR SMART; SM00082; LRCT; 4.
 DR SMART; SM00013; LRNT; 4.
 DR SMART; SM00369; LRR_TYP; 18.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS00022; EGF_1; 9.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
 DR PROSITE; PS50506; LRR_TYPICAL; 5.
 DR EGF-like domain.
 FT NON TER
 SQ SEQUENCE 1618 AA; 176732 MW; BF62DFD047B034E0 CRC64;
 Query Match 19.5%; Score 334.5; DB 4; Length 1618;
 Best Local Similarity 25.1%; Pred. No. 1.4e-14;
 Matches 97; Conservative 65; Mismatches 121; Indels 103; Gaps 9;
 QY 10 VPDRDF---EPSPGVPFRCQCHLRYVOCSDLGDKVPRKDPDPTLLDLONNKITE 65
 DB 579 IPGTEDYQINSECNSDVVCPEKRCCEANVVECSSIKLTKEIPERIPQSTAEIRLNNEISI 638
 QY 66 IK-DGDFPKLKNLHALILVNNKISKVSPGAFPLVKLERLYLSKNQLKELEPKPKTQE 124
 DB 639 LEATGMFKLTHLKKNLSNNKVSIEIDGAFEGAASVELHTANQLSISGMRGLDG 698
 QY 125 LRA---HNEITKYKVTENGINQIVIELGTNPDKSGIENGAFQGMKKLS----- 173
 DB 699 LRTMLRNRRISCIHNSFTGLRVRLSLYDNOITT--VSPGAFDTLQSLSTINLAMP 756
 QY 174 ----- 173
 DB 757 FNCNQCLAMLGWLRRKRIYVGNPRCONPDLRQIPLODVAFPDFRCEGEGGCLPRP 816
 QY 174 -----YIRIADNITSIPQGLPPSLTELHLDNKISRDAASLKGNNLAKGL 222
 DB 817 QCPQECACLDIVVRCNSNHLALPKGIPKNTVELYLDNQFTLV-PQLSTFKYIQVLDL 875
 QY 223 SFNSISAVNGSLANTPHLREHLDNKLTRVP---GGLAEHKYIOVYVYLNHNISVYG 278
 DB 876 SNNKISSLSNSSFNNMSQTLTLLSYNALQCIPLAFGL---RSLRLSLHGNDISTLQ 932
 QY 279 SSDFCPPGHNTKKASYSGVSLFSNPV 304
 DB 933 EGIF-----ADVTSLSHLAIGANPL 952
 RESULT 16
 Q8WV2 PRELIMINARY; PRT; 674 AA.
 ID Q8WV2;
 AC Q8WV2;
 DT 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DR Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018370; AAH18370.1; -
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 2.
DR PROSITE; PS00119; PA2_ASP; 1.
KW Hypothetical protein.
SQ SEQUENCE 674 AA; 74087 MW; 38AB53F7243166CC CRC64;

Query Match 19.4%; Score 333; DB 4; Length 674;
Best Local Similarity 28.8%; Pred. No. 6,6e-15;

Matches 88; Conservative 59; Mismatches 103; Indels 56; Gaps 7;

QY 24 CPEPCCHLRVVOCSDLGLKVPKDLPPPTLLDQNNKITEIKDGFKNLKNLHALLIV 83
DB 54 CFSVCRCDNGFTYCNDRGLTSPADIPDATTIYLONNQINNA-GIPDLKT----- 104
QY 84 NKKISKVSFGAFTPLVKEERLYSKQQLKEPKMKPTLOELRAHENEITTKVAKTENG 143
DB 105 -----KYNVQVIYLYENDLDEFPINLRSLRELTLQNNVRTIARDSLARI 150
QY 144 NQMIYELGTNPILKSSINGEAFQKKLSYRIADNTITSIQGLPBLTEHLHDGKI 203
DB 151 PLEKELHLDNDSVTSVIEBDAFADSKQLFLSRNHLSPSGLPHTLEBLRLDLDNR 210
QY 204 SEVDASLKLNNIAKLGISFN-----SISAVDNGSLANTP----- 239
DB 211 STPLHAFGLNSLRVLVDGNILANQRIADDTFSLQNLTELSLVAN-SLAAPPLNLS 269
QY 240 -HIRELHLDNNKLTTRVP-GGLAEHKYIQVYVYLNHNNISVVGSDFCPPGHNTKASYS 297
DB 270 AHLQKLYLDNNAISHIPYNTLAKMRELRDLSSNNLTTL-----PRGLFDLGLAQL 323
QY 298 SLFSNP 303
DB 324 LIRNNP 329

RESULT 17

Q9DE02 PRELIMINARY; PRT; 120 AA.
AC Q9DE02;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DR Biglycan-like protein 3 (Fragment).
GN BGL3 OR BGL3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.
ON NCBI_TaxID=7955;
RX (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247823; AAG40158.1; -
DR ZFIN; ZDB-GENE-010131-5; Bg13.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_Typ;
DR Pfam; PF00560; LRR; 4.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
FT NON TER 1
FT NON TER 120
SQ SEQUENCE 120 AA; 13569 MW; 37A302FB59F7696 CRC64;

Query Match 19.3%; Score 330; DB 13; Length 120;
Best Local Similarity 52.9%; Pred. No. 9,8e-16;

Matches 63; Conservative 27; Mismatches 29; Indels 0; Gaps 0;

QY 44 KVPKDLPPDTLLDQNNKITEIKDGFKNLKNLHALLIVNKKISKVSPGAFPLVKLR 103
DB 1 KVPKDLPPDTLLDQNNKITEIKDGFKNLKNLHALLIVNKKISKVSPGAFPLVKLR 60
QY 104 LYLKQKLEPKMKPTLOELRAHENEITTKVAKTENGLOMIVIELTNPILKSSGIR 162
DB 61 LHLSTNLTQMBENLPISVQSLRLHDNKISRLPKGAFKGMIDLNVLELSANPIANS 119

RESULT 18

Q9WB5 PRELIMINARY; PRT; 1531 AA.

AC Q9WB5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE SLT1L.
GN SLT1L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster/ICR;
RX MEDLINE=99365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse SLT1 family: secreted ligands for ROBO expressed in
RT patterns that suggest a role in morphogenesis and axon guidance.";
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144627; AAD44758.1; -
DR HSSP; P00743; ICCF.
DR MGD; MGI:1315203; Slit1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR003645; FcIN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR00372; LRR_Nterm.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.

Query Match	19.2%	Score 328.5	DB 11	Length 1531
Beat Local Similarity	24.5%	Pred. No. 3.3e-14		
Matches	94	Conservative	65	Mismatches 127; Indels 97; Gaps 8
QY	10	VPDDRDF---	EPSLGPVCPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNNKITE	65
DB	495	IPGTEDYHINSECTSDVACPHKRCCEASVVECSLSLKSIPRIPOSTTELRLNNNEISI	554	
QY	66	IK-DQDFNKLKMLHLLIIVNNKISKVSPPAFPIPVYLELYLSKNOLEKLPREMPRTLOE	124	
DB	555	LEATGLFKKLSLKLKINISNNVSEIETEDTFFGASVSSEHLITANOLESIRSGMFRGLDG	614	
QY	125	LRA---HNEETKVKKVFENGNOHIVIELGNPLKSGSILENGAFQGMKLS-----	173	
DB	615	LRTLMRLNNRIRISCHINDSTGLRNVRLSLYDNNHTT--ISQAFPTLOALSTLNLANP	672	
QY	174	-----	173	
DB	673	FNCNCHLSWGLDMLRRKRLVITGNPRQNDPIRLQIPLQVAFDPDFRCGQEEVGLPRP	732	
QY	174	-----YIRADNTITSIPQGLPSPSLTEHLNDKSKISRYDAASLKLGNLAKLGL	222	
DB	733	QCPQECACLDIVRRCSNKKLQALPKGIPKQVTELYLDGQFTLV-EGOLSTFKYLDLVDL	791	
QY	223	SFNSISAVDNGSLANTPHLRBLHLDNKKLTRYPG-GLABHYIQVYLIHNNNISVYGSSD	281	
DB	732	SNKKISSLSNSSFNTMSQTLTLLSTNALOCIPPLAFQRLRSIRLSTLHGNDVSTLOEGI	851	
QY	282	FCPPGHNTKKASVSGVSLFSPNV	304	
DB	852	F-----ADVTLSHLAIGANPL	868	
RESULT 19				
Q9WB4				
AC	Q9WB4	PRELIMINARY;	PRT; 1523 AA.	
ID	Q9WB4			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)		
DE	SL1r3	(Fragment).		
GN	SL1r3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Swiss Webster/ICR.			
RX	MEDLINE=99365246; PubMed=10433822;			
RA	Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.,			
RT	"The mouse Slrt family: secreted ligands for ROBO expressed in			
RL	patterns that suggest a role in morphogenesis and axon guidance."			
RL	Dev. Biol. 212:290-306(1999).			
EMBL	AF144629; AAD44760.1; --			
HSSP	P01132; 1EGF.			
DR	MGD; MG1:1315202; Sl1t3.			

```

DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR006207; Cys_knoc_C.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002049; laminin_EGF.
DR InterPro: IPR001791; laminin_G.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00008; EGF_9.
DR Pfam: PF00054; laminin_G; 1.
DR Pfam: PF00560; LRR; 19.
DR Pfam: PF01463; LRCT; 4.
DR Pfam: PF01462; LRRT; 4.
DR PRINTS: PRO0010; EGFLOOD.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00041; CT; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00282; lamc; 1.
DR SMART: SM00082; LRCT; 4.
DR SMART: SM00013; LRRT; 4.
DR SMART: SM00369; LRR_Typ; 7.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00022; EGF_1; 9.
DR PROSITE: PS01186; EGF_2; 7.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS50025; LAM_G_DOMAIN; 1.
DR PROSITE: PS50056; LRR_TYPICAL; 5.
KW EGF-like domain.
FT NON TER 1523
SQ SEQUENCE 1523 AA; 167711 MW; F43A3F3E016C4BFC CRC64;

Query Match 19.1%; Score 328; DB 11; Length 1523;
Beet Local Similarity 24.9%; Pred. No. 3,5e-14;
Matches 99; Conservative 53; Mismatches 124; Indels 122; Gaps 7.

QY 21 GP---VCFRCQCHIRVYQSCDGLGIDKVPKLPEDTTLDDIQQNKITEIKQGFKNLKNL 77
DB 28 GPAAACPTKCTCGAASVDCGGLGIRAVPRGI PRNAERLDDRRNNITRTKQDFAGLKNL 87
QY 78 HALIVNNKISKVSPGAFPLVYKLERLYLSKNOLKELEPKM---PKTQELRAHENEIT 133
DB 88 RVLHEDQVSIIERGAFQDQKQLERLKNKKQVLEELIPQSTPK-LTRLDISENQIQ 146
QY 134 KVRKVTENGILQMIVIELGTNPILKSSGIENGAFOGMKKLSYIRLADTNI----- 182
DB 147 GIPKAFPGVGVGNLQDDNNHI--SCIEDGAFALRLDELITLNNNISRLVTSFNHM 204
QY 183 ----- 182
DB 205 PKIRTLRLSHNLYCDCHLAWLSPDLRQRRTIGQFTLLCMAEVHLGFSVADYQKKEVYCP 264
QY 183 -----TSIDQGLPRSLTEHLQNKTSRYDA 208
DB 265 GPHEBAPACNANSISCPSACSCSNNIYDCRKGGLTEIPANIPGEGIVERLRLEONSTKSIIPA 324
QY 209 ASLKGANLIALKGLSFNSISAVDNGSLANTPHLEIHLDNKKLTFVPGGLAEHKY-IQV 267
DB 325 GAFYQYKGLKRIKIDISKNOISDIPADPAFGGLKSLTSLVLYGNKKITEIPAGLPDGLVSLQL 384
QY 268 YLHNNNISVGSDFCPGHANTKASYSGVSLFSNPVQ 305
DB 385 LLNANKINCIRVNTF-----QDIQNLNLTSLYDNKIQ 416

```

[illegible]

QY	174	-----	173
Db	673	FNCHNCQIAMLGDWIKRKRIYVTGNPRCONPDFLRQIPLQDVAEPDFRCBGEQEVGCLPRP	7322
QY	174	-----YIRIADINITSIPQGLPSPSLTEHLHDGKISRYPDASLKGJLNNLAKLG	2222
Db	733	QCPQECALDIPVRCSSNKHQLQMPGIGIPSNVVELYIDGQFTLV-PGQLSTFKYLOLVDL	7911
QY	223	SFNSISAVDNGSLANTPHLRBLHLNNKILTRVP-----GGIASHKYYIQVYVLIHNNNISVVG	2781
Db	792	SNNKISSLSNSSEFTNMQSLTTLTILSYNMLQCCPLPAFQL-----RSRLRLSLHNDVSTLQ	8481
QY	279	SSDFCPPEGHNTKKASYSYGVSLEFSNPV	304
Db	849	EGIF-----ADVTSLSHLAIGANPL	868
RESULT	21		
ID	088280	PRELIMINARY;	PRT; 1523 AA.
AC	088280;		
DT	01-NOV-1998	(TREMBLrel. 08. Created)	
DT	01-NOV-1998	(TREMBLrel. 08. Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23. Last annotation update)	
DE	MEGF5.		
GN	MEGF5.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid:10116;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;		
RX	MEDLINE=96360089; PubMed=9693030;		
RA	Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.,		
RT	"Identification of high-molecular-weight proteins with multiple EGF-		
RT	like motifs by motif-trap screening";		
RL	Genomics 51:27-34 (1998).		
DR	EMBL; AB011531; BAA32461.1; -.		
DR	HSSP; P01132; 1EGF.		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR006207; Cys_knot_C.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR001438; EGF_II.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR002049; Laminin_EGF.		
DR	InterPro; IPR001791; Laminin_G.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR000372; LRR_Nterm.		
DR	InterPro; IPR003591; LRR_typ.		
DR	Pfam; PF00008; EGF_9.		
DR	Pfam; PF00054; Laminin_G; 1.		
DR	Pfam; PF00560; LRR_19.		
DR	Pfam; PF01463; LRRCT; 4.		
DR	Pfam; PF01462; LRRNT; 4.		
DR	PRINTS; PR00010; EGFBLD.		
DR	PRINTS; PR00011; EGFLAMININ.		
DR	PRINTS; PR00019; LEBURICRPT.		
DR	SMART; SM00041; CT; 1.		
DR	SMART; SM00179; EGF_CA; 1.		
DR	SMART; SM00282; LamG; 1.		
DR	SMART; SM00082; LRRCT; 4.		
DR	SMART; SM00013; LRRNT; 4.		
DR	SMART; SM00369; LRR_TYP; 9.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.		
DR	PROSITE; PS01185; CTCK_1; 1.		
DR	PROSITE; PS01225; CTCK_2; 1.		
DR	PROSITE; PS00022; EGF_1; 9.		
DR	PROSITE; PS01186; EGF_2; 7.		
DR	PROSITE; PS01187; EGF_CA; 2.		
DR	PROSITE; PS50025; LAM_G_DOMAIN; 1.		

DR PROSITE; PS50506; LRR_TYPICAL; 5.
 KW EGF-like domain.
 SQ SEQUENCE 1523 AA; 167767 MW; 6CE1B7AF244478B CRC64;

Query Match 19.1%; Score 327; DB 11; Length 1523;
 Best Local Similarity 24.9%; Pred. No. 4,2e-14;
 Matches 99; Conservative 53; Mismatches 124; Indels 122; Gaps 7;

QY 21 GP--VCPFCQCHLRVYQCSDLGLDKVPKDLPPDTLLDLQNNKITEIKDGFKNLKNL 77
 DB 28 GPPAACPFKCTCSAASVDCGGLRAVPRGIRPNERLDLDNNITRIKMGFTGLKNL 87
 QY 78 HALIIVNNKISKSPGAFPLVLERLYLSKNQKELPERM---PKTLOELRAHNEIT 133
 DB 88 RYVHLLEDNOVSVERGAFODLKQLERLRNKNLQVLPFLFQSTPK-LTRLDLSENOIQ 146
 QY 134 KYRKFVNGLNQIVLELGNPLKSSGIENGAFQGGKSLYIRIADTNI----- 182
 DB 147 GLPKAFPRGVTVKNIQLDNNHI--SCIEDGARLRALDELITLNNNNISRIILVTSFNMW 204
 QY 183 ----- 182
 DB 205 PKIRTRLHSNHLVCDCHLAWLSDWLRQRRTIGQFTLCAPVHLRGSVADVQKKEVCP 264
 QY 183 -----TSIPQGLPPLSTELHLDGKKISRVD 208
 DB 265 GPHSEAPACNANSLSCPSACSCNNIVDCGKGLTEIPANLPBGIVIRLEQNSIKSIPA 324
 QY 209 ASLKGANNLAKLGLSFNSISAVNGSLANTPHLRELDNNKILTRVPGGLAEHKY-IQV 267
 DB 325 GAFIQYKRLKRIISKNQISDIPADPFGKLSLTSVLVGNKITEIPKGLFDSGLVSLQL 384
 QY 268 YLHNNNISVVGSSDFCPGHNTKKASVGSVLSFNSVQ 305
 DB 385 LNNANKINCIRVNTF-----QDLQNLNLSTLVNDKQLQ 416

RESULT 22

ID Q020204 PRELIMINARY; PRT; 1440 AA.

AC Q020204;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE F40E10.4 protein.
 GN F40E10.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleoderinae; Caenorhabditis.
 OC NCB1_TaxID=6239;
 RN NCB1 SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 investigating biology";
 RT Science 282:2012-2018(1998).
 RL [3]
 RN SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z69792; CA93668.2;
 DR EMBL; AL022270; CA93668.2; JOINED.
 DR EMBL; AL022270; CAB63434.1;
 DR EMBL; Z69792; CAB63434.1; JOINED.
 DR HSSP; P00740; IEDM.
 DR WormRep; F40E10.4; CE23711.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR006207; Cys_knot_C.

DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR01881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR01611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Tyr.
 DR Pfam; PR00008; EGF_7.
 DR Pfam; PR00054; laminin_G_1.
 DR Pfam; PF00560; LRR_18.
 DR Pfam; PF01463; LRRCT; 4.
 DR Pfam; PF01462; LRRNT; 4.
 DR PRINTS; PR00010; EGFBIOD.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00179; EGF_Ca; 2.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00082; LRRCT; 4.
 DR SMART; SM00013; LRRNT; 4.
 DR SMART; SM00369; LRR_Typ; 7.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS00022; EGF_1; 7.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
 DR PROSITE; PS50506; LRR_TYPICAL; 4.
 KW EGF-like domain.
 SQ SEQUENCE 1440 AA; 161942 MW; 0B5D198645D73670 CRC64;

Query Match 19.0%; Score 325; DB 5; Length 1440;
 Best Local Similarity 26.0%; Pred. No. 5.3e-14;
 Matches 107; Conservative 62; Mismatches 119; Indels 124; Gaps 13;

QY 24 CFFRCQCHLRVYQCSDLGLDKVPKDLPPDTLLDLQNNKITEIKDGFKNLKNLILV 83
 DB 17 CPACVCVDRVTSVCGQQLTEVPQNIPTIRLDLDNNEITIKGPNDFSLNMLKALQLM 76
 QY 84 NKKISVSPGAFPLVLERLYLSKNQKELPERM----- 118
 DB 77 DNOIYVTHNQSFSVLFQKRLSRIRIRLDPDNVFNQNLKULTHLDLSENDITVVSDAQ 136
 QY 119 --PKTLOELRAHNEI-----TKRKATFNGNQIVIE-----LGTN 154
 DB 137 QGPFLFLVNLNKNHIFCLENNVSSWSLEVLTLNG-NRLTFEPSPARROLDLFNN 195
 QY 155 P-----LKSSGIE--NGAF--QGMKLSY----- 174
 DB 196 FNNCDRLMKRWKLEKAGQNKVCATPLNLQSSSIELDQKFMTCGNNRRRRYKTC 255
 QY 175 -----IRLDNITISIPQGLPPLSTELHLDGKKISRVDASLKGANNLAK 219
 DB 256 TAEICPLCTCTGTYVDCDSGLTYVPTLPSTTEIRLEQNISSIPSHSPFNLNKLT 315
 QY 220 IGLSFNSISAVNGSLANTPHLRELDNNKILTRVPG---GLAEHKYIQVYLIHNNIS 275
 DB 316 LDISKNITIEIPKAFGLAHNLHTLVLYGNNTIDLSKDTFEGIGS---IQTLNLANNQ 372
 QY 276 VV--GSSDFCPGHNTKKASVGSVLSFNPVQWYIEIOPSTFRCVYVRSALQ 325
 DB 373 CIRGTFPHVP-----KLSMLSLYNDIK--SISVTFQNLSTLSLTLH 414

RESULT 23

ID Q09E336 PRELIMINARY; PRT; 1512 AA.

AC Q09E336;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE S11c2.

Qy 279 SSDCPGPHNTKASYSVGLFSNPV 304
 Db 849 EGIF-----ADVTSLSHLAIGANPL 868

RESULT 27

ID 094813 PRELIMINARY; PRT; 1529 AA.
 AC 094813;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Slt-2 protein.
 GN Slt-2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=99033071; PubMed=9813312;
 RA Itoh A., Miyabayashi T., Ohno M., Sakano S.
 RT "Cloning and expressions of three mammalian homologues of drosophila
 RT slt suggest possible roles for slt in the formation and maintenance
 RT of the nervous system."
 RL Brain Res. Mol. Brain Res. 62:175-186(1998).
 DR EMBL; AB017168; BAA5185.1; -.
 DR HSSP; P00743; ICCF.
 DR Genew; HGNC:11086; Slt2.
 DR InterPro; IPR000152; AaX_hydroxyl.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR00645; EGF-like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR00372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Cyp.
 DR Pfam; PF00008; EGF_9.
 DR Pfam; PF00054; laminin_G; 1.
 DR Pfam; PF00560; LRR; 17.
 DR Pfam; PF01463; LRRCT; 4.
 DR Pfam; PF01462; LRRNT; 4.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00274; FOLN; 2.
 DR SMART; SM00282; LAMG; 1.
 DR SMART; SM00082; LRRCT; 4.
 DR SMART; SM00013; LRRNT; 4.
 DR SMART; SM00369; LRR_TYP; 8.
 DR PROSITE; PS00010; AaX_HYDROXYL; 2.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS00022; EGF_1; 9.
 DR PROSITE; PS01186; EGF_2; 7.
 DR PROSITE; PS01187; EGF_3; 7.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
 DR PROSITE; PS05006; LRR_TYPICAL; 5.
 DR EGF-like domain.
 KW EGF-like domain.
 SQ SEQUENCE 1529 AA; 169869 MW; 5D19C5E7FD461BA CRC64;

Query Match 18.8%; Score 322; DB 4; Length 1529;
 Best Local Similarity 25.2%; Pred. No. 9.3e-14;
 Matches 104; Conservative 62; Mismatches 129; Indels 118; Gaps 12;

Qy 10 VPDDRDEPSPISGP-----VCPFRQCCHLRVQCSDLGLDKVPKDLPPDTTLIDLONNKI 63
 Db 486 IPGTEDYRSKLSGDCPADLACEKRCRCGTTVDGNSQNLANKIPHIPIQYTAELANNNP 545
 Qy 64 TEIK-DGDFKILKILHILVNNKISKVSPGAFPLVYLERLYLSKNQKELPERMPKYL 122

Db 546 TVLEATGIFFKLPOLRKINFSNNKITDIEGAFEGASGVNELLTNRLENVQKMKGL 605
 Qy 123 QELRA-----HENETKRYKTYFNGLNOMIYELGTNP 155
 Db 606 ESKLTMLRNSRNTTCVGNDSFGLSVRLISLYDNOITTVAPGAFDTLSLTNLINLP 665
 Qy 156 -----LKSGIENGAPQ-----GMKLS 173
 Db 666 FNCNCYIAMIQEWLRKKRIYVGNPROCKPFFLEKIPIDVAIQDFTCDGNDNDSCEPLS 725
 Qy 174 -----YRIADNTITSIPQGLPSLTSLHDGNTKISVDAASLGLNNLAVLGL 222
 Db 726 RCFTECTCLDTVVRCSKGLKVLPGKIPRDVTELYLDGNQFTLV-PRKLSYKHLTLIDL 784
 Qy 223 SPSISAVDNGSLANTPHLELHDNNKILTRVP-----GGLAEKTYIOVYLNHNNTISVNG 278
 Db 785 SNNRISTLSNQSSNNQTLLTLISYNRLKCIPTPTFDGL--KSLRLSLHGNDSIVV- 840
 Qy 279 SSDCPGPHNTKASYSVGLFSNPV-----QYMEIOPSTFRC 316
 Db 841 -----PGAFNDLSLSHLAIGANPLXCDCNMQWLSDWVSEYKE--PGIARC 866

RESULT 28

ID 081V47 PRELIMINARY; PRT; 376 AA.
 AC 081V47;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Similar to fibromodulin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R;
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC035281; AAB35281.1; -.
 SQ SEQUENCE 376 AA; 43178 MW; DC19D5E6724AB04 CRC64;

Query Match 18.8%; Score 321.5; DB 4; Length 376;
 Best Local Similarity 29.9%; Pred. No. 1.7e-14;
 Matches 85; Conservative 55; Mismatches 119; Indels 25; Gaps 8;

Qy 8 PEVDDRDPEPSPISGPVCPFRQC---HLRVQCSDLGLDKVPKDLPPDTTLIDLONNKIT 64
 Db 68 PSPDPDPD-----CPQECDCPPNPFTAMYCDNNNLKYL-FVPSRMKYVVFQNNQIT 118
 Qy 65 EIKDGPKNILKILHILVNNKIS--KVSQAFPLVYLERLYLSKNQKELPERMPKYL 122
 Db 119 SIQGVFDNATGILWIALHNGQITSDKVGKVSQKRLHRLRYLDHNNLTFRMGPLPRSL 178
 Qy 123 QELRAHENETKRYKTYFNGLNOMIYELGTNPLKSGIENGAFQGMKLSYRIADNTI 182
 Db 179 RELHLHDNQLSRPNNNALEGLENTYALYDHNELIQYGV---SSMRGLRSLLILDSTNHL 235
 Qy 183 TSIPQGLPSLTSLHDGNTKISVDAASLGLNNLAKGLSFSNISAVDNGSLANT--P 239
 Db 236 RKVPDGLPSALBEDLYMEHNNVYVPSYFGAPKRLVYRSHSLT--NNGLASNTNNS 293
 Qy 240 HLERLHDNNKILTRVQGLAEKTYIOVYLNHNNTISVNGSDRC 283
 Db 294 SLLELDLSYNQLOKIP---PVNTNLEMLYDGNRINEFSSISC 334

RESULT 29

ID 09DE37 PRELIMINARY; PRT; 1515 AA.
 AC 09DE37;
 ID 09DE37;
 AC 09DE37;


```

DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE SLIT3.
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Michigan;
RA Yeo S.Y., Okamoto H.;
RT "Zebrafish slit3 homolog.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210320; AAG36772.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 18.
DR Pfam; PF01463; LRRT; 4.
DR Pfam; PF01462; LRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00082; LRR; 4.
DR SMART; SM00082; LRRT; 4.
DR SMART; SM00369; LRR_TYP; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 5.
KW EGF-like domain.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD11277D18D5B CRC64;

Query Match 18.6%; Score 318.5; DB 13; Length 1515;
Best Local Similarity 22.4%; Pred. No. 16e-13;
Matches 100; Conservative 53; Mismatches 133; Indels 161; Gaps 7;

QY 24 CEFRCQCHLRVYQCSGLGDKVPKOLPPDTLLDLONNKITEIKQDFKLNKLNHALILV 83
DB 24 CPHKSCSGSHVDCQQAFAKTVPRGIPRAVERLDLDRNNITITKVDPSGLNKLRLVHLIE 83
QY 84 NKKIKSVSGAFTPLVYKLERLYLSKQKLELPKPKMT--LOELRAHENEITTKRATVF 140
DB 84 NNQISVIERGAFEGKQKLERIRINRRLQVLPBLFQSTTKLSRLDLSNQIDAVPRKAF 143
QY 141 NGINQWIVTELGNPLKSGIENGAFQKKGKSYIRIADTNI----- 182
DB 144 RGIITVYKLIQLDNSNI--SCIEDGAFRALRDLEILTNNNNTITLPLSSFNMPKLRITR 201
QY 183 ----- 182
DB 202 LHSNNLHCDCHLSWLSDWLRQRGLAPFTQCMAPAHMRGLANVDVQKREFTCTGPEVETEP 261
QY 183 ----- -TSIQGLPPSLTEHLNDNKISRDVAASLKL 214

```

```

DB 262 RSCAQATTCPACTCANNITVDCRRKGLTEIRPANIPEGIVETRLDQNMINKIPAGAFSTY 321
QY 215 NNIAKIGLSFNSISAVDNGSLANTPLRLHLNDNKLTRVPGGL----- 258
DB 322 KKLKRIDLSKQISIEADAFGLSLTSLVYGNKIAEIPKGLFGLVSLQLLLLNANK 381
QY 259 -----AEKTYQVYVYLLHNNNISVVGSSDFP-----FGHTKKS 293
DB 382 INCLRWNTFKLDQNLNLSLNDNKLQTSKGLFAPLRALKTLHLAQNPFMCDCHLKMILAD 441
QY 294 YSGVSLFSNPVQYWEIOPSTPFCVYR 320
DB 442 Y-----LFQNP-----LETSGARCSHPR 459

RESULT 30
O991B9
AC O991B9 PRELIMINARY; PRT; 1521 AA.
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster/ICR;
RA MEDLINE=99365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse Slit family: secreted ligands for ROBO expressed in
RT patterns that suggest a role in morphogenesis and axon guidance.";
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF14628; AAD4759.1; -.
DR HSSP; P00743; 1CCF.
DR MGD; MGI:1315205; SLIT2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003645; FOIN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRT; 4.
DR Pfam; PF01462; LRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00274; FOIN; 2.
DR SMART; SM00282; LAMG; 1.
DR SMART; SM00082; LRRT; 4.
DR SMART; SM00082; LRRT; 4.
DR SMART; SM00013; LRNT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 5.
KW EGF-like domain.
SQ SEQUENCE 1521 AA; 168769 MW; 97DCA361578978E4 CRC64;

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 11:38:24 / Search time 75 Seconds

(without alignments)
918.490 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713

Sequence: 1 VEASGIGPEVDDRDPEPSL.....QPSTFRVCVYSAIQGNKY 329

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1713	100.0	329	US-10-004-176-6
2	1709	99.8	360	US-09-764-875-804
3	1365.5	79.7	354	US-10-319-130-20
4	984.5	57.5	369	US-10-319-130-19
5	979	57.2	368	US-10-236-031B-68
6	979	57.2	368	US-10-177-293-99
7	943.5	55.1	379	US-09-866-028-2
8	943.5	55.1	379	US-09-944-449-2
9	943.5	55.1	379	US-09-944-457-2
10	943.5	55.1	379	US-09-944-862-2
11	943.5	55.1	379	US-09-945-587-2
12	943.5	55.1	379	US-09-945-015-2
13	943.5	55.1	379	US-09-944-396-2
14	943.5	55.1	379	US-09-944-097-2
15	943.5	55.1	379	US-09-944-432-2

16	943.5	55.1	379	US-09-943-762-2	Sequence 2, Appl1
17	943.5	55.1	379	US-09-944-654-2	Sequence 2, Appl1
18	943.5	55.1	379	US-09-943-851A-2	Sequence 2, Appl1
19	943.5	55.1	379	US-09-944-413-2	Sequence 2, Appl1
20	943.5	55.1	379	US-09-944-403-2	Sequence 2, Appl1
21	943.5	55.1	379	US-09-944-896-2	Sequence 2, Appl1
22	943.5	55.1	379	US-09-944-929-2	Sequence 2, Appl1
23	943.5	55.1	379	US-09-944-907-2	Sequence 2, Appl1
24	943.5	55.1	379	US-09-944-884-2	Sequence 2, Appl1
25	943.5	55.1	379	US-09-944-852-2	Sequence 2, Appl1
26	943.5	55.1	379	US-09-943-780-2	Sequence 2, Appl1
27	943.5	55.1	379	US-10-137-870-328	Sequence 328, App
28	943.5	55.1	379	US-10-140-018-328	Sequence 328, App
29	943.5	55.1	379	US-10-140-021-328	Sequence 328, App
30	943.5	55.1	379	US-10-140-274-328	Sequence 328, App
31	943.5	55.1	379	US-10-140-471-328	Sequence 328, App
32	943.5	55.1	379	US-10-140-807-328	Sequence 328, App
33	943.5	55.1	379	US-10-140-922-328	Sequence 328, App
34	943.5	55.1	379	US-10-140-924-328	Sequence 328, App
35	943.5	55.1	379	US-10-140-926-328	Sequence 328, App
36	943.5	55.1	379	US-10-141-698-328	Sequence 328, App
37	943.5	55.1	379	US-10-141-702-328	Sequence 328, App
38	943.5	55.1	379	US-10-141-704-328	Sequence 328, App
39	943.5	55.1	379	US-10-142-421-328	Sequence 328, App
40	943.5	55.1	379	US-10-142-432-328	Sequence 328, App
41	943.5	55.1	379	US-10-142-767-328	Sequence 328, App
42	943.5	55.1	379	US-10-143-033-328	Sequence 328, App
43	943.5	55.1	379	US-10-144-994-328	Sequence 328, App
44	943.5	55.1	379	US-10-145-628-328	Sequence 328, App
45	943.5	55.1	379		

ALIGNMENTS

RESULT 1
US-10-004-176-6
Sequence 6, Application US/10004176
Publication No. US20030124152A1
GENERAL INFORMATION:
APPLICANT: Pang, Danny Z.
TITLE OF INVENTION: Use of decorin in a cosmetic or dermatological composition
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/004,176
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 6
LENGTH: 329
TYPE: PRT
ORGANISM: Human
US-10-004-176-6

Query Match 100.0%; Score 1713; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.6e-152;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VEASGIGPEVDDRDPEPSLGPVCPFRQCHRYVQCSDDLGLDKVPKLPDPTLLDION	60
DB	1	VEASGIGPEVDDRDPEPSLGPVCPFRQCHRYVQCSDDLGLDKVPKLPDPTLLDION	60
QY	61	NKITEIKGDDPKNNKNNHALILVNNKTSKVSFGAFPLVKLERLYLSKNQKELPEKMPK	120
DB	61	NKITEIKGDDPKNNKNNHALILVNNKTSKVSFGAFPLVKLERLYLSKNQKELPEKMPK	120
QY	121	TLQELRAHNEITTKRYKTFFNGLNQMTVIELGTNPDKSSGIENGAFOQKKLSYIRIADT	180
DB	121	TLQELRAHNEITTKRYKTFFNGLNQMTVIELGTNPDKSSGIENGAFOQKKLSYIRIADT	180
QY	181	NITSPQGLPSTLTSLHDGKTKISRVDAASIKGLNNLAKLGISFNSISAVNNGSLANTPH	240
DB	181	NITSPQGLPSTLTSLHDGKTKISRVDAASIKGLNNLAKLGISFNSISAVNNGSLANTPH	240

QY 241 LRELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 300
DB 241 LRELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 300
QY 301 SNPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
DB 301 SNPVOYWEIQPSTFRVCVYRSAIQLGNYK 329

RESULT 2

US-09-764-875-804
; Sequence 804, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 804
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-875-804

Query Match 99.8%; Score 1709; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 6,9e-152;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 33 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 92
QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 121
DB 93 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 152
QY 122 LOELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIADTN 181
DB 153 LOELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIADTN 212
QY 182 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHL 241
DB 213 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHL 272
QY 242 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 301
DB 273 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 332
QY 302 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
DB 333 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 360

RESULT 3

US-10-319-130-20
; Sequence 130, Application US/10319130
; Publication No. US20030148351A1
; GENERAL INFORMATION:
; APPLICANT: Henry, Stephen P
; APPLICANT: Mayne, Richard
; APPLICANT: Hook, Magnus
; TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SEQUENCES OF ASPORINS
; FILE REFERENCE: 12740.0234.NPUS02
; CURRENT APPLICATION NUMBER: US/10/319,130
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/341,537
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-319-130-20

Query Match 79.7%; Score 1365.5; DB 12; Length 354;
Best Local Similarity 79.9%; Pred. No. 1.2e-119;
Matches 262; Conservative 28; Mismatches 33; Indels 5; Gaps 1;

QY 2 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 32 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 86
QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 121
DB 87 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 146
QY 122 LOELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIADTN 181
DB 147 LOELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIADTN 206
QY 182 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHL 241
DB 207 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHL 266
QY 242 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 301
DB 267 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLHNNNISVVGSSDFCPGHNTHKASYSVSLP 326
QY 302 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
DB 327 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 354

RESULT 4

US-10-319-130-19
; Sequence 19, Application US/10319130
; Publication No. US20030148351A1
; GENERAL INFORMATION:
; APPLICANT: Henry, Stephen P
; APPLICANT: Mayne, Richard
; APPLICANT: Hook, Magnus
; TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SEQUENCES OF ASPORINS
; FILE REFERENCE: 12740.0234.NPUS02
; CURRENT APPLICATION NUMBER: US/10/319,130
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/341,537
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-319-130-19

Query Match 57.5%; Score 984.5; DB 12; Length 369;
Best Local Similarity 57.6%; Pred. No. 7.4e-84;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQ 59
DB 40 EASGIGPEVDDRDPEPSIGVPCFRCCCHLRVVOCSDLGLDKVPKDLPPDTLLDLQ 99
QY 60 NNTTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 119
DB 100 NNTTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVYLERLYLSKNQKELPERKMPKT 159
QY 120 KTLQELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIAD 179
DB 160 KTLQELRAHENEITKRVKVTENGILNOMIVIELGTNPDKSSGIEENGAFQGMKLSYIRIAD 218


```

; Sequence 2, Application US/09866028
; Patent No. US20020058309a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION DATA REMOVED - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-2

```

```

Query Match      55.1%; Score 943.5; DB 9; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

```

QY 11 PDRDDEPSLGPVCPFRCCGLHRYVQCSVDLGLDKVRKDLPPDTLLDQNNKTEIKDGD 70
DB 61 PRSHFFPFDLPFCPCFCQCCYSRVHCSDLGLTSVPFNIPDTRMLDQNNKTEIKEND 120
QY 71 EKLNKLNHALIYNKSKSPGAFPTLVLELYLSKNOLKELPEKMPETLOELAHEN 130
DB 121 EKELTSYGLILNNKTKTHPAFLTKKLRLRYSHNDLSIPNLPRSLAMELRHEN 180
QY 131 EITKRVKVTENGNNOMIVIELGTPNPKSGIENGAFQMKKLSYIRIADNINISPOGAP 190
DB 181 KVKKIQKQDTPKGNALHVLMSANPLDNGIEPGAEGV-TVHIRIAEKALTSVPGGLP 239
QY 191 PSLTEHLADGNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHIRELHLDNNK 250
DB 240 PTLLEHLADYNKISTVELDEPKRYKELQRLGIDGNKTTDIEGSLANIIPVREIHLNNK 299
QY 251 LTVPGGLAHKTIQVYVILNNNISVYGSDFPCPGHNTKKASYGVLSFNPVQWEIQ 310
DB 300 LKKIPSGLPKLTQIIFLHNSNLSIARVGVDPFPTVPMKKKSLYSALISFNNPVKWEQ 359
QY 311 PSTFRCYVRSATOLGNY 328
DB 360 PATFRCVLSRMSYQLGNF 377

```

```

RESULT 8
US-09-944-449-2
; Sequence 2, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey

```

```

; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095

```

;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 26, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 2
;; LENGTH: 379
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-449-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRRFESLGPVCPFCOCHRVVQCSDLGDKVPKPLPPTLLDQNNKTEIKXGD 70
DB 61 PRSHFFPDLFPWCFPGCCISRVVHCSDLGTSVPTNIPPTRLDQNNKTEIKXND 120
QY 71 FKNLNLHALILVNNKISKVSPGATPLVKLERLYSKNQLKEPEKPKTLOBRAHEN 130
DB 121 FKGLSLVGLILNNKRLKIRHKAPLTTRKRLRLVLSNQSLSEILNPKSLAEIRHEN 180
QY 131 EITKRAKTYFNGLNOMIYIELGTNPLKSSGIENGAPQCKSLSYRIADVTNITSIPQGLP 190
DB 181 KVKTKQKOTFKGMNLAHLTEMSANPLDNNGLIEPGAPEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSLELHLDGNKISVVDASLKGILNNLAKLGISPRISAVNDSLANTPHLRELHLDNNK 250
DB 240 PTLLEHLADYNKISTVELDEDFRYEQLRLGIGNNKITDIENGSLANIPEVAEHLNENK 299
QY 251 LTRVVGGLAEHKYIOVYILHNNNISVVGSSDFCPGHNTKASYSGVSLFSPVOYMEIQ 310
DB 300 LKTIISGLPELKYLOIITLHNSIARVGVNDPCITVPKMKSLYSALISLNNPVKYMENQ 359
QY 311 PSTRCVYVRSALQIGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 9
US-09-944-457-2
;; Sequence 2, Application US/09944457
;; Patent No. US20020110859A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerltsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kijavlin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel

;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P254BP1C1
;; CURRENT APPLICATION NUMBER: US/09/944.457
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,286
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/114,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-457-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDEPSPGVPFCPCQCHRVQCSDLGLDKVKEKDLPPDTTLDDLQNNKITEIKDGD 70
 DB 61 PRSHFPDLFPWCPCGOCYSRVHVCSDLGLTSVPTNIPEDTRMDLQNNKIKEIKEND 120
 QY 71 ENLKLHLHLLVNNKISKVSPGAFPLVYKLERLYSKQQLPEKPMPTTLOELPAHEN 130
 DB 121 FGLGLSYGLILNNKLTGTHHPAFLTTKRLRLYSHQSLSEIPLNLPKSLAEIRIHEN 180
 QY 131 EITKVKVTFNGNLGNMIVIELGTNPFKSGIENGAFQKKKSLYIRIADTNITSIPQGLP 190
 DB 181 KYKKIKQDTFKGNMAHVEHMSANPLDNNIGIEGAEV-TVHIIAEKGLTSVKGAP 239
 QY 191 PSTELHLDGNKISRVAASLKLGNLAKGLSFNSISAVDNGSLANTPHLEHLDNNK 250
 DB 240 PTLLEHLNKNKISTVELEDFKRYKELQRLGLNKNITIDENGLNIPRVREIHLENK 299
 QY 251 LRRVPGLAHKIKQVYVLLHNNNISVVGSSDFCPGHNTKKASVGSVLSFNVQYWEIQ 310
 DB 300 LKKIPGSLPELKYLIQIIFLHNSIAVGVDFCPVPMKKSLYSALSIFNPKYKWEQ 359
 QY 311 PSTFRCVYVSATQGNV 328
 DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 10
 US-09-944-862-2
 Sequence 2, Application US/09944862
 Patent No. US20020115145A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltisen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavlin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944, 862
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866, 028
 PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067, 411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069, 334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069, 335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069, 278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069, 425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069, 696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069, 694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069, 702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069, 870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069, 873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068, 017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070, 440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074, 086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074, 092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075, 945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112, 850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113, 296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146, 222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216, 021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218, 517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254, 311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020115145A1, December 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020115145A1, December 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRPEPGLGVCPFCQCHLRVYCCSDGLDVKVPKDLPPDTTLDDONNKITEIKOD 70
DB 61 PSHHFPPLPFMCPCGQCCYRVHCSDLGTSVPTNIPDTMLDLONNKIKEIKEND 120
QY 71 FNLKMLHALIVNNKISVSPGAFPLVLEKLYLSKNQOLPEKMKPTLOELRAHEN 130
DB 121 FKGTLSTVLGLINNNKLTIRPKAFPLTKKRLRLVSHQLEIPNLKSLAEIRIHEN 180
QY 131 ETKVRKRTFENGLQMIYELGTNPDKSGIENGAFQCKKLSYRIADTNTISIPQGLP 190
DB 161 KVKKIQKOTFKGMALHVLKEMSNPLDNNIGPGEV-TVFHIRIAEAKLTSPVKGLP 239
QY 191 PSLTEHLHGKISRDAASLKGNNLAKLGSFNSISAVDGSALNPHLEHLDDNK 250
DB 240 PTLLEHLDDYKISTVELEDPRKRYKELQRLGKNNKITDIENGSLANIPREIHLNNK 299
QY 251 LTRVGLAEHKYIGVYVLIHNNNISVSSDFCPGHNKTKKASYSVSLFSNPVOYWEIQ 310
DB 300 LKKIPSGLPKLYLQIFLHNSIARVGVNDFCPTVPKMKSLYSALSFNNPVKYMENQ 359
QY 311 PSTRCYVRSALQGNV 328
DB 360 PATFRCLSRMSVOLGNF 377

RESULT 12

US-09-945-015-2

Sequence 2, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Auelin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tomas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-015-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRPEPGLGVCPFCQCHLRVYCCSDGLDVKVPKDLPPDTTLDDONNKITEIKOD 70
DB 61 PSHHFPPLPFMCPCGQCCYRVHCSDLGTSVPTNIPDTMLDLONNKIKEIKEND 120

QY 71 FKNLKNLHALLLVNKKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKTLQELRAHEN 130
Db 121 FKGLTSLYGLLNNKKLTKHPKAFLLTKKLRLYLSHNSQSEIPLNPKSLAEIRIHEN 180
QY 131 EITVRKATFNGLNOMIYIELGTNPILKSSGIENGAFQOMKLSYRIRADNTITSIPQGLP 190
Db 181 KVKKIQKOTFGKGNALHLEWMSANPLDNGIEPGAEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLHLDGNKISRVDAASLKGILNLAAGLSFISIAVDNGSLANTPHLREHLDNKK 250
Db 240 FTLEHLDHYNKISVLEDEDERKRYELQRLGKNNKIDIEGSLANTPRAREHLENNK 299
QY 251 LTRVPGSLAEKHYIQVYVLAHNNISVSGSDPCPEGHNTKCAYSVGSLSFSPVQWYEQ 310
Db 300 LKKIPSGHPELKYYQIIFHSNSIARVGVNDFCTVPKMKSLYSALISLFNNPVKXWEMQ 359
QY 311 PSTRCYVVRSAIQGNV 328
Db 360 PATFRCVLSRMSVOLGNF 377

RESULT 13.
US-09-944-396-2
Sequence 2, Application US/09944396
Patent No. US20020132981A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Batson, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Auelin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PCL
CURRENT APPLICATION NUMBER: US/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132981A1,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132981A1,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-396-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDDBEBSLGPVCPFCQCLARVQCSDLGLDKVYKPLPDDTLDD:ONNKITIKQGD 70
Db 61 PRSHFPFDPDLFPWCPFGQCYSRVHGSGLTSTVPIVPTDTRMLD:ONNKIKIKEND 120
QY 71 FKNLKNLHALLLVNKKISKVSPGAFPLVKLERLYLSKNQKELPEKMPKTLQELRAHEN 130
Db 121 FKGLTSLYGLLNNKKLTKHPKAFLLTKKLRLYLSHNSQSEIPLNPKSLAEIRIHEN 180
QY 131 EITVRKATFNGLNOMIYIELGTNPILKSSGIENGAFQOMKLSYRIRADNTITSIPQGLP 190
Db 181 KVKKIQKOTFGKGNALHLEWMSANPLDNGIEPGAEGV-TVFHIRIAEAKLTSVPKGLP 239

Db 360 PATFRCVLSHMSVOLGNF 377

RESULT 15

US-09-944-432-2

Sequence 2, Application US/09944432
Patent No. US20020142419A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavini, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tuma, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,762
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,286
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 26, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-432-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

11 PDRDPEPSLGPVCPFCOCHLRVOCSDGLKVPKDPDPTLDDLNKKITEIDGD 70
61 PRSHFPFPLPFCPCPCOCYSRVHCSGLSVPTNIFPDTRMLDQNNKIKELKEND 120
71 FKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPTLOELRAHEN 130
121 FKGLTSLYGLILNNKTKLHPKAPLTTKKLRRLYLSHNGLSLPLNLPKSLAEIRHEN 180
131 EITKRVKVTNGANQIVIELGTPNPKSSGIEGAGQMKLSYIRIADNITISPGGLP 190
181 KVKKIQDTPKGNNAALVLEMSANPLDNNGIEGAGEGV-TVPHIRIAEAKLTSVPGGLP 239
191 PSTLEHLIDGNKISRYDAASLKGNNLAKGLSPNSISAVDNGSIANTPHRLHLDNNK 250
240 PTLLEHLIDNKNKSTYELERFKRYKELORGLGNKITTDLNENSLANIPIVREHLHLENNK 299
251 LTRVPGGLAEHKYLOVYTLANNNISVVGSSDFCPGPHNTKASVGSVSPVQVWEIQ 310
300 LKKIPSGLPKLTGLIIFLHSNSIARVGVNDPCPTVPKMKSLYSALSLFNNPVKYMWQ 359
311 PSTFRCTVYSALQAGNY 328
Db 360 PATFRCVLSHMSVOLGNF 377

RESULT 16
US-09-943-762-2
Sequence 2, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltzen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gueney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavini, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/943,762
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-943-762-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFEPSLGPVCFPCQCHLRVQCSDLGI:DKVPKDLPPDTLLDLONNKITEIKGD 70
 DB 61 PRSHFPFDLPFMCFCGQCYSRVHCGDLGTVSPNTIPDTRMLDLONNKIKIKEND 120
 QY 71 FKNLKNLHALLVNNKISKVSPGAFPTVYKLERLYLSNQKELPEKPKPTLOELRAHN 130
 DB 121 FKGLTSLYGLILNNKIKIPKAFLLTTKRLRRLYSNQLSEIPLNPKSLAEIRIHEN 180
 QY 131 EITKVRKVTPLNGLOMYTEIGTNPDLKSSGTENGAFQGMKLSYRIADTNTISIPQGLP 190
 DB 131 KYKIKQKTFKGMALHVLKSNANPLDNGIEPQAFESV-TVFHRIKAEKLTSPKGLP 239
 QY 191 PSLTEHLIDGNKISRVDASLKGILNLAAGLSFNISAVDNGSLANTPHIRELHLDNNK 250
 DB 240 PTLLEHLIDYNNKISVLEDEPKRYKELQRLGIDNNKIIDINGSLANIPIVREIHLNNK 299
 QY 251 LTRVPGGLAEKTYQVYVILNANNISVVGSSDPFCPPGANTKASISGVSLEFSPVQYWEIO 310
 DB 300 LKIKPSGLPELKYQIIFLHNSIARVGVNDPCTVPKMKSLYSALISLFNNPVKYMEO 359
 QY 311 PSTPCVYVRSALQDQVY 328
 DB 360 PATFRCVLSRMSVQDQNF 377

RESULT 17
 US-09-944-654-2
 Sequence 2, Application US/09944654
 Patent No. US20020142959A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltzen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijaviv, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,654
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: NO. US20020142959A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: NO. US20020142959A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-654-2
 Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 11 PDDRRFEESLGPVCFRCOCHLRVQCSDLGDKVPKLPPTTLDDI:ONNKITEIKOSD 70
 61 PRSHFPDPDLPFPCPCGQCYSRVVCSDLGTSVPTNIPDTRMLD:ONNKIKKIKEND 120
 71 PNLKNTLALILVNNKISKVSPGAFPTPLVKLERLYSKNOULKEPEKPKTLOEIRAHEN 130
 121 FKGLTSLVGLIANNKLT/KIRPKAF/LTKLRRLYLSNQLSEITLNP/KSLAEIRIHEN 180
 131 EITVRYKVTENGLOMIVIEIETNP/LKSSGIENGAFQGMKKLSYRIADNTITSIPQGLP 190
 181 KVKIKIOKOTFGKGMNALHTLEMSANPLDNNNGIEPGAFEGV-TVFHIRIAEAKLTSVKGIP 239
 191 PSUTLHLDNKKISVNDASLKGMLNKLAKLISFISIAVNDGSLANTPHLRRLDNNK 250
 240 PTLLEHLHDYNKISVLEDEPRRYKEIQLRIGGNKKIYDINGSLANTPRVEIHLNNK 299
 251 LTRVPGIAEAKHYIOVVLIHNNNISVVGSDPCPPGHNTKASVSGSLFSNPVOYWEIO 310
 300 LKKTSGPELKITLDOIIFLHNSIARVGVNDPCFVPPKKSLSYSAISLFNNPVKWEIQ 359
 311 PSTFRCVYVRSALIQYNT 328
 360 PATFRCVLSRMSVQGNF 377
 Db
 RESULT 18
 US-09-943-851A-2
 Sequence 2, Application US/09943851A
 Patent No. US20020150976A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijaviv, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT FILING DATE: 2001-08-30
CURRENT APPLICATION NUMBER: US/09/943, 851A
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/09/866, 028
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020150976A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020150976A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-943-851A-2
Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRPEPSLGPVCPFCQCHLRVQCSDLGDKVPEKDIAPPDTLLDLQNNKITEIKGD 70
Db 61 PRSHFPFDLPFCPCGCGCYSVVACSDGLTSVPTNIPDTRMDLQNNKIKEIKEND 120
QY 71 FKRLKYLALILVNNKISKVSRCAPPLVYLERLYISKQQLKELPKMPKXTLOELPAHEN 130
Db 121 FKGLTSLYGLILNNNDLTHHPKAFLTTRKRLRLYLSHQLSSEIPNLKSLAEIRIHEN 180
QY 131 EITKVKVTFENGINOMIVLELGTNPKSSGIENGARQMKKLSYTRIDNTNLSIPQGR 190
Db 181 KVKKIKQDTPFKMNAHLVEMSNPDDNNGIEGAEVQ-TVPHILAEKQLSVKGLP 239
QY 191 PSITELHLDGNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTPHRLHLDNNK 250
Db 240 FTLLEHLHDYNNKISTVELEDPFKRYKELQRLGNNKITIDENGSLANIRVREIHLNNK 299
QY 251 LRVPGSLAEKTIQVYVYHNNNISVSGSDPCPGHNTKYSKYSVSLFSPNVOYWEIQ 310
Db 300 LKKIPGLPELKYTLQITFLHSNSIARVGVNDCPTVPKMKKSLYSALISFNNPVKYMWQ 359
QY 311 PSTPRCVYVRSAILQGNV 328
Db 360 PATFRCVLSRMSVQLGNF 377
RESULT 19
US-09-944-413-2
Sequence 2, Application US/09944413
Patent No. US2002015604A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroli, Ellen
APPLICANT: Gerdtisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411

PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,684
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,226
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-413-2
 Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity .55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 Db 11 PDDRPERPSLGPVPCPCQCHLAVVCCSDGLDKVPDLPPTTLIDLNKKITEIDGD 70
 61 PRSHFFPFDLPVPCPCQCYRVRHCSDDLGLTVSPNIPFDFTMDLQNNKKEIKEND 120
 Db 71 FKULKNLHALILVNNKSKVSGAFPLVLERLYISKNLKELPEKMPLOELRAHEN 130
 121 FKGLTSLYGLILNNKTKLHPKAFITTKLRLYLHSHNQLSEIPLWIPSLAEIRHEN 180
 Db 131 EITKRVKVTENGINQIVIEIGTNPVLSKSGIENGAFQGMKKLSTYRIADTNTISIPQGLP 190
 181 KVKKIQDQTFKGMVAHLVLEMSANPLDNGIEPCAFGV-TVFHRIAEAKLTSVPKGLP 239
 Db 191 PSLTEHLIDGNKISRVDAAALKGLNMLAKIGLSPNSISAVDNGSLANTPHLEHLDNKK 250
 240 PTLLEHLIDYNNKISTVELDEPKRYKELQRLGNNKLTIDENGLANI PVREIHLNKK 299
 Db 251 LTRVPGSLAEKRYIQVYVYLNHNNISVYSSDFCPGHNTKASVSGVLSFNPQVWEIQ 310
 300 LKPIPSGLPELKIYQITFLHSNSIARVGVNDFCTVPRMKKSLYSALSFNNPKYEMQ 359
 Db 311 PSTERCYVRSATOLGNV 328
 360 PATRCVLSRWSVQLGNF 377
 Db
 RESULT 20
 US-09-944-403-2
 Sequence 2, Application US/09944403
 Patent No. US20020165143A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gettisen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavich, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,403
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US200201651431member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US200201651431member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-403-2
 Query Match 55.1%; Score 943.5; DB 10; Length 379;

Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 11 PDRDFEBSLGPVCFRQOCHLRVQCSDLGDKPKPULPPTTLDDLNKITERKOD 70
 DB 61 PSHFPPEDLPFCPCFGQCYSVVHCDLGLTSPVPIPFTRMLDLONNIKIKIKEND 120
 QY 71 FNLKRLHALILVNNKISKVSPGAFPLVTKERLYISKQULKELEPKMKPTLOELRAHEN 130
 DB 121 FGLSLSVGLILNNKRLTKIHPKALFTTKGLRLLYLSHNSQLSEIPLNPKSLAEIRIHEN 180
 QY 131 ETTVKRYTENGILNOMIVIELGTNPLKSSGIEBNGAPQMKSLSYRIADNTITSIPQGLP 190
 DB 181 KVKKIOXOTFKGMNLAHLVEMSANPLDNNGIEPGAFEGV-TVFHIRIAKLTSPVKGLP 239
 QY 191 PELTEHLHDNKSISVDASLKLGNLAKLGISFISISAVDNGSLANTPHLEHLDNNK 250
 DB 240 PTLLEHLHDYNKISTVELEDFRKYRELRLGIGNKRTIDTENGSLANTPVEIHLENNK 299
 QY 251 LTRVPGSLAEHKYIOVVYLLHNNNISVGSSDPCPGHNTKSKASYSVSLFSNPVOYWEIO 310
 DB 300 LKKIPSGLEPKLTIQIIFLHSNISARVGVNDPCFTVPKPKKSLYSNISLFPNPKYWEIO 359
 QY 311 PSTFRCCYVRSALIQAGNY 328
 DB 360 PATFRCVLSRMSVQLGNF 377
 RESULT 21
 US-09-944-896-2
 Sequence No. Application US/09944896
 Patent No. US20020168715A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltzen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gueney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kljavin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944.896
 PRIOR FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,966
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020168715A, member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020168715A, member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/00520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO: 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-896-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5,4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEPSLGPVPCPCOCHLWVQCSDLGDKVPEKDLPPDTTLADLQNNKITEIKDGD 70
 DB 61 PSHHPRPDLFPKPCPCGCCYSRVAVCSDLGLTSVTNPIDPRMDLQNNKIKELKEND 120
 QY 71 FKNLKULHALLVNNKISKVSQPAFTPLVLELYLSKQQLPEKMPKTLQELPAHEN 130
 DB 121 FKGLTSLYGLILNNKLTIKHPAFLLTKKGLRLYLSHQLSSEIPLNLPKSLAELRIHEN 180

QY 131 EITKRVKTFNGLNQMIYIELGTNP LKSSGIENGAFQGMKLSYIRIADTNTISIPQGLP 190
 DB 181 KVKIKQDTPKGMALAHVLEMSANPLDNGIEPBAFEV-TVPHIRIKALTSVPEKLP 239
 QY 191 PSLTEHLIDGNKISRVDASIKGLNLA KIGLSFNSSIAVDNGSIANTPHLREHLDNKK 250
 DB 240 FTLLIEHLIDYKISTVELEDFKRYKELO RLGIDGNKKTIDINGSLANIPIVREIHLNKK 299
 QY 251 LTRVPGGLAEHKYIQVYVILHNNNISVYSSDFPCPEGHNTKRAVSQSVLFSNPVQWMEIQ 310
 DB 300 LKKIIPSGLPKELYQIIFLHNSNIA RVGVNDPCTVPKPKSLYSALSIFNNPVKYMWQ 359
 QY 311 PSTFCVYVRSALQDQNY 328
 DB 360 PATRCVLSRMSVQDGNP 377

RESULT 22
 US-09-944-944-2
 Sequence 2, Application US/09944944
 Patent No. US20020173463A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gertlisen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Aunein
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kljavin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548PICI
 CURRENT APPLICATION NUMBER: US/09/944,944
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092

```
/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/075,945
/ PRIOR FILING DATE: February 25, 1998
/ PRIOR APPLICATION NUMBER: 60/112,850
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 60/113,296
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 60/146,222
/ PRIOR FILING DATE: July 28, 1999
/ PRIOR APPLICATION NUMBER: PCT/US98/19330
/ PRIOR FILING DATE: September 16, 1998
/ PRIOR APPLICATION NUMBER: PCT/US98/25108
/ PRIOR FILING DATE: December 1, 1998
/ PRIOR APPLICATION NUMBER: 09/216,021
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 09/218,517
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 09/254,311
/ PRIOR FILING DATE: March 3, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: June 22, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: September 15, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28409
/ PRIOR FILING DATE: No. US20020173463A member 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: No. US20020173463A member 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28301
/ PRIOR FILING DATE: December 1, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: December 16, 1999
/ PRIOR APPLICATION NUMBER: PCT/US00/03565
/ PRIOR FILING DATE: February 11, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: February 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: March 2, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: March 30, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: May 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: July 28, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: December 1, 2000
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: February 28, 2001
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 2
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-944-944-2
```

```
Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEPSLGPVCPFCOCCHLRVVOCSDLGLDKVPDLPPTLLDLONNKITEIKODG 70
DB 61 PRSHFPPDLFPMPGCPGOCYSRVVHCSDGLTSVPTNIPFPTRMIDLONNKIKEIKEND 120
QY 71 FKNLKNLHALLVNNKISKVSPGAFPTLVKLERLYSKNQLKELPEKMPKTLQELRAHEN 130
DB 121 FKLTLSTGLYLILNNKLTIKHPKAFITTKQLRLYLSHNLSEIPLNLPKSLAEKRIHEN 180
QY 131 EITKVRKVTENGLOMIVIELGNPLKSSGIEGAFQGMKLSYIRIADTNITSTIQGLP 190
DB 181 KVKKIKQDTPFKMNLHLVLEMSANPLDNNGIEGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLEHLDNKISRVDASLKGILNMLAKGLSPNSISAVDNGSLANTPHLREHLHDNNK 250
DB 240 PTLLEHLHDYNNKISTVELEDFKRYKELQRLGKNNKITIDENGLANTIPRVEIHLHNNK 299
```

```
QY 251 LTRVPGSLAEHKYIQVYVLIHNNNISVVGSSDFCPGHNTRKASYSVSLFSNPOYWEIQ 310
DB 300 LKKIPSGLELTKLQIIFLHNSIARVGVNDPCPTVPKAKKSLYSALISLFPNVKXWEMQ 359
QY 311 PSTFRCVVRSALQIGNY 328
DB 360 PATFRCVLSRMSVOLGNF 377

RESULT 23
US-09-944-929-2
/ Sequence 2, Application US/0944929
/ Publication No. US20020197612A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Botstein, David
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gerltzen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul
/ APPLICANT: Grimaldi, Christopher
/ APPLICANT: Guirney, Austin
/ APPLICANT: Hillan, Kenneth
/ APPLICANT: Kijavlin, Ivar
/ APPLICANT: Napier, Mary
/ APPLICANT: Roy, Margaret
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Wood, William
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P2548P1C1
/ CURRENT APPLICATION NUMBER: US/09/944, 929
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: 09/866, 028
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 2
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-944-929-2
```

```
Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEPSLGPVCPFCOCCHLRVVOCSDLGLDKVPDLPPTLLDLONNKITEIKODG 70
DB 61 PRSHFPPDLFPMPGCPGOCYSRVVHCSDGLTSVPTNIPFPTRMIDLONNKIKEIKEND 120
QY 71 FKNLKNLHALLVNNKISKVSPGAFPTLVKLERLYSKNQLKELPEKMPKTLQELRAHEN 130
DB 121 FKLTLSTGLYLILNNKLTIKHPKAFITTKQLRLYLSHNLSEIPLNLPKSLAEKRIHEN 180
QY 131 EITKVRKVTENGLOMIVIELGNPLKSSGIEGAFQGMKLSYIRIADTNITSTIQGLP 190
DB 181 KVKKIKQDTPFKMNLHLVLEMSANPLDNNGIEGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLEHLDNKISRVDASLKGILNMLAKGLSPNSISAVDNGSLANTPHLREHLHDNNK 250
DB 240 PTLLEHLHDYNNKISTVELEDFKRYKELQRLGKNNKITIDENGLANTIPRVEIHLHNNK 299
QY 251 LTRVPGSLAEHKYIQVYVLIHNNNISVVGSSDFCPGHNTRKASYSVSLFSNPOYWEIQ 310
DB 300 LKKIPSGLELTKLQIIFLHNSIARVGVNDPCPTVPKAKKSLYSALISLFPNVKXWEMQ 359
QY 311 PSTFRCVVRSALQIGNY 328
DB 360 PATFRCVLSRMSVOLGNF 377
```

RESULT 24

US-09-944-907-2

; Sequence 2, Application US/09944907
; Publication No. US20020198147A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
 ; APPLICANT: Batstein, David
 ; APPLICANT: Batson, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kijavlin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,907
 ; CURRENT FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 2
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-944-907-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;

Best Local Similarity 55.0%; Pred. No. 5,4e-80;

Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFBPSLGVPFCPCCHLRVQCSDLGDKVPKDLPPDTLLDLDONNKITEIKGD 70
 DB 61 PRSHFFPDLFPMPGFCGOCRSRVHCSDDLGLTSVPTNIPTDTMLDLDONNKIKEIKND 120
 QY 71 FKNLKNLHALILVNNKISKVSPGAFPLVKERLYLSKNOLKEPEKPKTLOELRAHEN 130
 DB 121 FKGLTSLYGLILNNKLTKEHPKAPLTTKRLRLYLSNQSLSEIPLNPKSLAEARHEN 180
 QY 131 EITKRAKTYFNGLNQMIYIELGTNPLKSSGIENGAFQGMKLSYRIADNTITSIPQGLP 190
 DB 181 KYKKIQKDTFKGMNALHYLEMSANPLDNGIEPGEV-TVFHRIAEAKLTSVPKGLP 239
 QY 191 PSTLEHLDGNKISRVDASIKGLNNLAKLGLSFNSISAVNGSLANTPHLEHLDNNK 250
 DB 240 PTLLEHLDYKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTPRVREHLENNK 299
 QY 251 LTRVPGGLAEHKYIQVYILHNNNISVVGSSDFPCPGHNTKASVGSVLSFNPVOYWEIQ 310
 DB 300 LKKIPSGLPBELKYLIIFLHNSIARVGVDPCFTVPKMKKSLYSALSLFNNPVKYMWQ 359
 QY 311 PSTFRCVYVRSALIOLGNY 328
 DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 25

US-09-944-884-2

; Sequence 2, Application US/09944884

; Publication No. US20030077698A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
 ; APPLICANT: Batstein, David
 ; APPLICANT: Batson, Dan

; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kijavlin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,884
 ; CURRENT FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 2
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-944-884-2

Query Match 55.1%; Score 943.5; DB 11; Length 379;

Best Local Similarity 55.0%; Pred. No. 5,4e-80;

Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFBPSLGVPFCPCCHLRVQCSDLGDKVPKDLPPDTLLDLDONNKITEIKGD 70
 DB 61 PRSHFFPDLFPMPGFCGOCRSRVHCSDDLGLTSVPTNIPTDTMLDLDONNKIKEIKND 120
 QY 71 FKNLKNLHALILVNNKISKVSPGAFPLVKERLYLSKNOLKEPEKPKTLOELRAHEN 130
 DB 121 FKGLTSLYGLILNNKLTKEHPKAPLTTKRLRLYLSNQSLSEIPLNPKSLAEARHEN 180
 QY 131 EITKRAKTYFNGLNQMIYIELGTNPLKSSGIENGAFQGMKLSYRIADNTITSIPQGLP 190
 DB 181 KYKKIQKDTFKGMNALHYLEMSANPLDNGIEPGEV-TVFHRIAEAKLTSVPKGLP 239
 QY 191 PSTLEHLDGNKISRVDASIKGLNNLAKLGLSFNSISAVNGSLANTPHLEHLDNNK 250
 DB 240 PTLLEHLDYKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTPRVREHLENNK 299
 QY 251 LTRVPGGLAEHKYIQVYILHNNNISVVGSSDFPCPGHNTKASVGSVLSFNPVOYWEIQ 310
 DB 300 LKKIPSGLPBELKYLIIFLHNSIARVGVDPCFTVPKMKKSLYSALSLFNNPVKYMWQ 359
 QY 311 PSTFRCVYVRSALIOLGNY 328
 DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 26

US-09-944-852-2

; Sequence 2, Application US/09944852

; Publication No. US20030083479A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
 ; APPLICANT: Batstein, David
 ; APPLICANT: Batson, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kijavlin, Ivar

```

: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,852
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 2
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-944-852-2

Query Match      55.1%; Score 943.5; DB 11; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFBBSLGPVCFPRCCCHLRVQCSDPLGLDKYVKDLPPTTLIDLQNNKITEIKOD 70
DB 61 PRSHFPFPLFPMCFPGCCGSRVHCSDLGILSVPTNIPPTRMIDLQNNKITEIKEND 120
QY 71 FRNLKMLALLIVNNKISKVSFGATPLVYKRLYLSKNQKELPEKPKTLOELRAHEN 130
DB 121 FRGLSLVGLILNNKLTIKHPKAFLLTKCLRLYLSHQSLSEIPLNPKSLAEIRIHEN 180
QY 131 EITVRKVTYFNGLNOMIVLELGNPLKSSGENGAFCQKKTSLYRIADTNTSLPQCLP 190
DB 181 KYKTKQXTFKMNLHYLWNSANPLDNNGIPEGAEGV-TVFHIRIAEAKLTSPKGLP 239
QY 191 PSLELHLDGNKISRVDAASLKLNNLAKLGLSFNSISAVDGSANTPPLRELDHNNK 250
DB 240 FTLELHLDYNNKISVLEDEDFRYKELQRLGKNNKIDIDENGSLANIPRAVEIHLNNK 299
QY 251 LTRVGGSLAEKHTIVVYLLHNNNISVVGSSDFCPGHNTKASYSVGLFSNPVOYWEIO 310
DB 300 LKKIPGSLPELKYLIQIIFLHSNSIARVGVNDPCFTVPKMKKSLYALSLENNPVAYWEMQ 359
QY 311 PSTFCVYVRSALIOIGNY 328
DB 360 PATFRCVLSRMSVOLGNF 377

RESULT 27
US-09-943-780-2
: Sequence 2, Application US/09943780
: Publication No. US20030096742A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Baton, Dan
: APPLICANT: Batstein, David
: APPLICANT: Perrata, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/943,780
: CURRENT FILING DATE: 2001-09-26

```

```

: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,286
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678

```


QY 71 FKMLKMLHALIIVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPPTLOELRAHEN 130
 DB 121 FKGLTSLYGLILNNKKTJTKHPKAFITTKLRRLYLSHNOISEIPLMIPKSLAELRIHEN 180
 QY 131 EITKRVKVTENGINOMIVIEIGTNPILKSGSIEGNGAFQGMKKLSYIRIADNINISIPQGLP 130
 DB 181 KVKKIQDQTKGNMNAHLVLEMSANPLDNNNGIEPAGFV-TVFHIRIAEAKLTSVPGKLP 239
 QY 191 PSTLHLDGNKISRVDASLKGILNNIADKLGLSFSNISAVDNGSLANTPHLRELHLDNNK 250
 DB 240 PTLLEHLHDYNNKISTVELDFPKRYKELQRLGLGNKKITDIENGSLANIPRVREIHLNNK 299
 QY 251 LTRVPGGLAEHKYIQVYVYLLHNNNISVSGSDFCPGHNNTKASYSVGLFSNPVQWEIQ 310
 DB 300 LKKIPGGLPELKYLIQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKXWEMQ 359
 QY 311 PSTFRCVYVRSALIQGNV 328
 DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 30

US-10-140-021-328
 ; Sequence 328, Application US/10140021
 ; Publication No. US20030138866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Geriltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tuma, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zhen
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C167
 ; CURRENT APPLICATION NUMBER: US/10/140,021
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 328
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-140-021-328

Query Match 55.1%; Score 943.5; DB 12; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEBGLGVCPPRCCHLRAVOCSDLGDKVPKDLPPTTLIDLONNKITEIKGD 70
 DB 61 FSHHPFPDLFPMPGCGQYGRVHSCDGLTSLVPTNIPPTRMIDLONNKIKEIKEND 120
 QY 71 FKMLKMLHALIIVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMPPTLOELRAHEN 130
 DB 121 FKGLTSLYGLILNNKKTJTKHPKAFITTKLRRLYLSHNOISEIPLMIPKSLAELRIHEN 180
 QY 131 EITKRVKVTENGINOMIVIEIGTNPILKSGSIEGNGAFQGMKKLSYIRIADNINISIPQGLP 190
 DB 181 KVKKIQDQTKGNMNAHLVLEMSANPLDNNNGIEPAGFV-TVFHIRIAEAKLTSVPGKLP 239
 QY 191 PSTLHLDGNKISRVDASLKGILNNIADKLGLSFSNISAVDNGSLANTPHLRELHLDNNK 250

DB 240 PTLLEHLHDYNNKISTVELDFPKRYKELQRLGLGNKKITDIENGSLANIPRVREIHLNNK 299
 QY 251 LTRVPGGLAEHKYIQVYVYLLHNNNISVSGSDFCPGHNNTKASYSVGLFSNPVQWEIQ 310
 DB 300 LKKIPGGLPELKYLIQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKXWEMQ 359
 QY 311 PSTFRCVYVRSALIQGNV 328
 DB 360 PATFRCVLSRMSVQLGNF 377

Search completed: February 9, 2004, 11:48:19
 Job time : 81 secs